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Thermodynamics of Polycaprolactone-water systems

Analysis of interactional issues by comparing ab-initio and molecular approaches with a classical lattice fluid theory of mixtures

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Contents

Abstract Polycaprolactone-water mixtures represent one of the most important polymer solutions with specific interactions in polymer science. Polycaprolactone (PCL) is an aliphatic polyester composed of hexanoate repeat units. It is a semicrystalline polymer with a degree of crystallinity which can reach 69PCL biodegrades within several months to several years depending on the molecular weight, the degree of crystallinity of the polymer, and the conditions of degradation. Many microbes in nature are able to completely biodegrade PCL. The amorphous phase is degraded first, resulting in an increase in the degree of crystallinity while the molecular weight remains constant. Then, cleavage of ester bonds results in mass loss. The polymer degrades by end chain scission at higher temperatures while it degrades by random chain scission at lower temperatures. PCL degradation is autocatalysed by the carboxylic acids liberated during hydrolysis but it can also be catalysed by enzymes, resulting in faster decomposition. While PCL can be enzymatically degraded in the environment, it cannot be degraded enzymatically in the body. PCL has uses in different fields such as scaffolds in tissue engineering, in long-term drug delivery systems (in particular contraceptives delivery), in microelectronics, as adhesives, and in packaging. Its wide applicability and interesting properties (controlled degradability, miscibility with other polymers, biocompatibility and potential to be made from monomers derived from renewable sources) makes PCL a very useful polymer if its properties can be controlled and it can be made inexpensively. This kind of mixtures are often used in biomedical applications where the property of to be biodegradable is necessary to adsorb and to avoid any clinical rejection of the implant. Water interactions in the polymer matrix are key rule in establishing the way and the time of scaffold reconstruction. Although many studies declare to be capable of handling hydrogen bond in polymer solutions, often this theory appears descriptive as matter of fact they deal with macroscopic nature of system and materials. A unifications between microscopic and macroscopic world is steal a matter of controversy. Start with thermodynamics theories allow us to calculate macroscopic properties of system in exam as accurately as possible. But much less accuracy can be found in the microscopic ones. Need to explore the phase space of a system, bring us to as a reasonable model as force field methods. Then we start exploring configuration space by trajectory provided by a molecular dynamics, This let to provide *macroscopic* properties and *microscopic*. Microscopic properties are the refined in a quantum fashion as the right configurations An Eos theory aim to describe and relate thermodynamic properties of matter. Aim of my research is to implement these theory describing polymer mixtures with specific interaction, clearly appear the need for a brief summary report of the theory jet elaborated.

Chapter 1

Mathematical model

In this chapter the mathematical model developed to characterize the behavior of polymer solutions varying environmental conditions will be described. In order to let the model naturally emerge from discussion, we will start describing briefly the two general kind of approaches: the macroscopic approach and the microscopic one. In section 1.1 we start to deal with the historical background of mathematical modeling.

1.1 Lattice Fluid theory

In nineteenth century the scientific world start the challenge to describe the world as the new law of physics are discovered. The development of thermodynamics models for complex fluids applicable over a wide range of contions is still an active and fashinating research area. Thermodynamics models based on statistical mechanics can be classified into lattice models and nonlattice models. Lattice theories of solutions in statistical thermodynamics are born aimed of describing fluids, they develop the idea of semi-crystalline liquid allowing the description of an hamiltonian made-up of the strictly approximation of Bragg-Williams. Fluid systems can be described using a regular lattice on the ground of the fact that the these systems exhibit a local order and significant interactions occurs at small scale range distances.

Bragg-Williams approximation The Bragg-Williams approximation in lattice fluid model, first developed to describe a simple magnetic system such as Ising model, can be easily used to describe the fluid solutions. It states the molecule or molecular fragment arranged in this semi-crystalline way.

first neighborhood approximation In this way the hamiltonian is very simplified and can be written as the summation of *first shell* interactions.

$$\Delta H = \sum_{ij} \sigma_i \cdot \sigma_j \tag{1.1}$$

Then the canonical partition function is written with only the *first interaction* energy term between any neighborhood lattice point. In the nineteenth century *regular* systems made up of molecule with different shape and volume

are described as having mixing entropy independent by any constituent molecular shape and volume.

In the 1936, at the Faraday Society, Fowler and Rushbrooke showed [41] that, with statistical analysis, monomer-dimer solutions, distributed on a lattice, where as semi-crystalline approximation stated monomer occupies one site and dimer occupies two site, have not *ideal* behavior. Beside the Fowler favorable idea to describe a liquid phase as point standing on a lattice, the two scientists showed the difference between ideal and non ideal solutions reside on the different molecule volume between solvent and polymer. Firstly we show this general model describing molecule bound to the lattice point, such as Ising problem, and then the second Bragg-Williams approximations with the aim to show the historical evolution of the theories.

1.1.1 Lattice Fluid

In statistical thermodynamics with the name of lattice fluid or cell fluid we identify a system where every part is confined to a lattice point and it can explore only a well defined neighborhood range of space, the cell volume. This is the same as the Ising Model introduced by Wilhem Leinz:

$$v = \frac{V}{M_0}$$

where V is the total volume of the solution and M_0 is the number of cells which the system is made, this latter can be equal to the number of molecules or parts system consists. Basic requirement is the these latter are spherical symmetry and to have very similar molecular volume.

This approximation allow to enumerate the various kinds of interactions between the molecules in the fluid and their numbers can be easily calculated. The number of provisions of large molecule that can appear are entirely described. Should be note that the model deals with condensed and incompressible matter at a given temperature. Each site is occupied and therefore the lack of vacant site determines the nonexistence of any pressure volume effect. The individual molecules that occupy the sites are considered to have an internal partition function that does not affected by the type of proximal molecule, they freely rotate and vibrate compared to their equilibrium position influenced only by the size of lattice cell. In case of solutions, to account the probability of an interchange between lattice points should be put in the system a term involving the entropy variation associated, called communal entropy. In a fluid lattice model, with interaction energy $J = \epsilon^*/\kappa_B T$ between neighborhood cell, the canonical partition function is

$$\mathsf{Z}_{lattice fluid} = \sum_{(e)} \exp(J \sum_{ij} e_i e_j) \tag{1.2}$$

where the summation is extend over all the possible configurations observing the sum rule reported:

$$\sum_{j=1}^{n} e_j = N.$$

Gran-canonical partition function is :

$$Z_{latticefluid} = \sum_{N=0}^{\infty} \Omega \exp^{\beta\mu N} \exp(J \sum_{ij} e_i e_j)$$

$$= \sum_{N=0}^{\infty} \Omega \exp(\beta\mu \sum_{i=1}^{N} e_i + J \sum_{ij} e_i e_j)$$

Alternatively one can describe the system through the use its Hamiltonian:

$$Z_{latticefluid} = \sum_{(e)} \exp - \frac{H}{\kappa_B T}$$

$$H = -\mu \sum_{i=1}^{N} e_i + \epsilon_* \sum_{ij} e_i e_j$$

Gran-canonical partition function is related to the pressure by the relation:

$$\ln Z_{latticefluid} = \frac{pV}{\kappa_B T}$$

$$\frac{pV}{\kappa_B T} = (\beta\mu \sum_{i=1}^{N} e_i + J \sum_{ij} e_i e_j) \times \ln \Omega$$

$$p = (\mu \sum_{i=1}^{N} e_i + \epsilon^* \sum_{ij} e_i e_j) \times \frac{\ln \Omega}{V} \tag{1.3}$$

This is *lattice fluid* state equation.

1.1.2 Bragg-Williams approximation

Although the exact and complete analytical solution, find in the previous paragraph can be found in mono dimensional case, do not exists any mathematical method to extend this latter one to bi- and tri-dimensional system. Then a need of a new approximation is clear. Bragg and Williams told to solve these latter kind of systems assuming the molecule to be randomly distributed among the lattice, this latter Bragg-Williams approximation is well known as *zero order approximation.*

$$g = \frac{M_0!}{(N_A!)(M_0 - N_A)!}$$

Bragg-Willliams theory can be used in solutions made up of molecule having the same volume and shape. As consequence any one point in the system can be exchanged with another one. This idea was first formulated by Pierre Weiss aimed to describe *ferro-magnetic systems* and then its extension to interacting fluid systems leads to this important result:

$$V^3 \propto (T_c - T)$$

1.1.3 Polymer Flory-Huggins theory

In every polymers solutions model should be keep in mind the great difference between polymer volume and any other ordinary molecule especially in that case of the solvent molecule. This aspect leads to a loss in symmetries needed to describe the molecule such as point on a lattice. The Flory-Huggins theory represents a seminal model in development of all the lattice fluid mean field theories that take into account the presence of polymeric species. The theory start over the assumption that a *lattice fluid* regular arrangement could describe a multicomponent fluid system. The tout-cour application of Fowler and Rushbrooke theory [41] cannot be done without the development due to Flory [18] and Huggins [25, 26], independently. He start to divide the polymer in a number of fragments, r, also called mer or segments, and then he confined this latter to a lattice site. Therefore a polymer, divided in an r number of *mer* occupying a single lattice point along a sort of *random walk* while the solvent only one. The regular lattice of cell's interactions can be described by the coordinations number of each cell, z, defining the total number of contacts allowed for each cell with the adjacent ones. Changing some variables have to be done as difference in the molecule occurs, molar fractions have to be substituted by volume fractions as:

$$\varphi_A = \frac{N_A}{N_A + rN_B} \qquad \varphi_B = \frac{rN_B}{N_A + rN_B}.$$

where N_i are the molar number of i-th component. We can define the total quantity of lattice points as $N_r = N_A + r \cdot N_B$.
The volume of the mixtures is assumed to be additive. Starting from the basic hypothesis, Flory calculated the change in the Gibbs free energy associated to the formation of the mixtures starting from the pure fluid components with the respect to its value in the pure fluid reference state. It is possible to deal with *mixing entropy* of the solvent with the polymer, starting with the Boltzmann entropy function.

$$S = k; ln\Omega \tag{1.4}$$

Assuming the entropy as a state function and after postulate the number of configurations, explored by the solvent molecule in the pure solvent, equal to one, $\Omega(N_A) = 1$, then we get:

$$\Delta S_{mix} = k \ln \frac{\Omega(N_A, N_B)}{\Omega(0, N_B)} \tag{1.5}$$

where Ω are the numbers of micro-state describing the system.
The quantity $\Omega(N_A, N_B)$ is the number of non-equivalent configurations which N_B polymers can occupy $r \cdot N_B$ lattice sites.

The polymer molecules are added successively to the lattice consisting of $N_r - rN_i$ free sites which are to be occupied by the solution. Suppose that i polymer molecules have been inserted previously at random in the lattice. There remains a total of $N_r - rN_i$ vacant cells in which to place the first *mer* of the molecule $i + 1$. Let z the coordination number of the lattice, there will be $z\frac{N_r - rN_i}{N_r}$ chances to find a neighborhood lattice point to accommodate the second *mer*. The expected number of cells available to the third segment will be $(z-1)\frac{N_r - rN_i}{N_r}$. For each succeeding segment, $r-2$, the expected number of

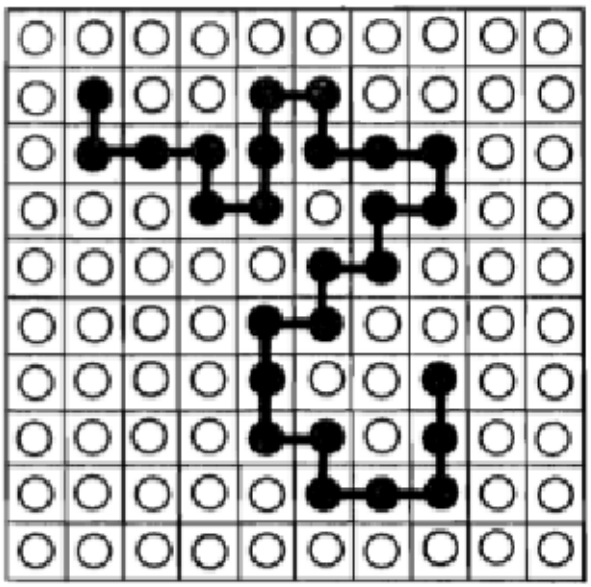

Figure 1.1: Segments of a chain polymer molecule located in the liquid lattice

permissible alternative assignments can be taken also as $(z-1)(1-\bar{f}_i)$, where $\bar{f}_i$ is the probability to find a occupied cell in the neighborhood. This latter number is upper limited by

$$\limsup(1-\bar{f}_i) = 1 - f_i = \frac{N_r - rN_i}{N_r}$$

Therefore the expectancy $\bar{f}_i$ will be somewhat more than provided the the occupation ofa cell selected at random. However, differences are estimated to be small [26]. Thus we have:

$$\omega_{i+1} = (N_r - r \cdot N_{B_i}) \cdot z(z-1)^{r-2} \cdot (1 - \frac{r \cdot N_{B_i}}{N_r})^{r_i - 1} \tag{1.6}$$

by replacing z with z-1, we get to:

$$\omega_{i+1} \simeq (N_r - r_i N_{B_i})^r \cdot (\frac{z-1}{N_r})^{r-1} \tag{1.7}$$

which may further approximated, with an imperceptible error, by

$$\omega_{i+1} \simeq \frac{(N_r - rN_{B_i}!)}{(N_r - rN_{B_{i+1}})!} \cdot (\frac{z-1}{N_r})^{r-1}. \tag{1.8}$$

Arrangements in which the sets of r contiguous lattice cells chosen for occupation by polymer molecule are identical but which differ only in the permutation of the polymer molecules over these sets would be counted as different in this enumeration scheme.

$$\prod^{N_B} \omega_i = N_B!\Omega \tag{1.9}$$

where ω_i represent the number of conformations the system can observe.

Substituting equation 1.8 in equation 1.9 we have:

$$\Omega = \left[\frac{N_r!}{(N_r - rN_B)!}N_B!\right]\left[\frac{(z-1)}{N_r}\right]^{N_B(z-1)} \tag{1.10}$$

Having supposed that each solvent molecule occupies only one cell lattice, we can assume each of them occupies in only one way the lattice, then the Ω calculated in equation 1.10 represents also the total number of configurations explored by the system, from which it follow that the configurational entropy of mixing is given by equation 1.4. Then, introducing the Stirling approximation in the equation 1.10, replacing N_r with

$$N_r = N_A + r; N_B$$

and with various simplifications, equation 1.4 yelds to:

$$S = -k\left[N_A ln\varphi_A + N_B ln\varphi_B\right] \tag{1.11}$$

$$+ kN_B\left[(r-1)\,ln\left(\frac{r-1}{e}\right)\right] \tag{1.12}$$

The first two term are the same describe the mixing of regular solution, the third represents the disordering process caused by the solvent. Although the polymer has changed its disorder in solvatation, the variation of this term is negligible [19].

Then:

$$\frac{\Delta S_{mixt}}{k} \simeq -N_A \ln\varphi_A - N_B \ln\varphi_B \tag{1.13}$$

The formation of the solution may be thinkned as chemical reaction in which bonds of a new type are formed at the expense of an equal number of the former two according to the stoichiometry equation:

$$\frac{1}{2}[A,A] + \frac{1}{2}[B,B] = [A,B].$$

If w_{ij} represent the energies associated with these pair contacts, or *bonds*, the change in energy for the formation of an unlike contact pair is

$$\Delta w_{AB} = w_{WB} - \frac{1}{2}\cdot(w_{AA} + w_{BB}) \tag{1.14}$$

Then, having a uniquely specified arrangement of the molecules in the solution described by the lattice fluid model, the number of unlike pair is totally specified. The heat of formation of that particular configuration from the pure component is

$$\Delta H_m = \Delta w_{12} p_{12} \tag{1.15}$$

In order to determine the average value of p_2 in a solution of given composition, we observe that a particular site adjacent to a polymer segment is occupied

by a solvent molecule is approximately equal to the volume fraction φ_A of the penetrant molecule in solution. The total number of *surface* contacts a polymer can done will be $z-2$ per number of *mer* plus two additional ones for the head and the tail of the molecule.

$$N_q = N_B \cdot [(z-2) \cdot r + 2] \tag{1.16}$$

In the limit of z very large, we can approximate this latter equation by

$$N_q \simeq N_B \cdot [z \cdot r]\,. \tag{1.17}$$

Hence the total number of unlike contacts become $zrN_B \cdot \varphi_A = zN_A \cdot \varphi_B$ and the heat of mixing may be expressed as

$$\Delta H_M = z\Delta w_{AB} N_A \varphi_B \tag{1.18}$$

this is the well known van Laar expression for the heat of mixing in any two-component system. This can generalized and we can recast in the form:

$$\Delta H_M = kT\chi_A N_A \varphi_B \tag{1.19}$$

where

$$\chi_A = \frac{z\Delta w_{AB} r_A}{kT}.$$

If the configurational entropy is assumed to represents the total entropy variation on mixing, the free energy of mixing is simply denoted by

$$\Delta F_M = \Delta H_M - T\Delta S_M \tag{1.20}$$

Then

$$\frac{\Delta F_{mix}}{kT} = -N_A \ln \varphi_A - N_B \ln \varphi_B + \chi_A N_A \varphi_B \tag{1.21}$$

In the calculation of the enthalpy associated to the formation of the mixtures, he introduces a dimensionless interaction parameter, χ. This is the only parameter used as fitting parameter when interpreting experimental data for binary systems.

In the case of a binary system the chemical potential change in the penetrating has the following expression:

$$\mu_1 - \mu_1^0 = RT\left[ln\varphi_1 + \varphi_2\left(1 - \frac{1}{r}\right) + \chi\varphi_2^2\right] \tag{1.22}$$

where μ_1 represents the chemical potential potential of the penetrating in the mixture, μ_1^0 the chemical potential of the pure penetrating at the same temperature, R the ideal gas constant, T the temperature, χ the interaction parameter, φ_1 the volumetric fraction of the penetrating and φ_2 the volumetric fraction of the polymer in the mixture.

Equilibrium solubility of a penetrating in a polymer can be modeled by equating the chemical potential of this latter in a pure liquid or vapor phase in contact with the polymer, assuming a negligible concentration of the polymer in the gas phase.

Flory equation of state

Despite the Flory-Huggins theory it is still a valid point of start understanding the thermodynamic of polymers blends, this theory exposes evident gaps in describing the changes related to the mixing volume. Key steps in improving this statistical-thermodynamic model was adopted, as described in some previous paragraph, based on the equation of state.

The first in order of time was Flory [39], followed by Sanchez and Simha. The thermodynamic variables in the statistical thermodynamics are obtained by a suitable the partition function that is ready to be more or less complex function of the system under examination. Described the partition function used by Flory takes thoughtlessness both contributions intra molecular, of a strictly chemical bond, both the intermolecular bonds.

$$Z = \Omega_*(g\upsilon^*)^{rNc}(\upsilon^{1/3} - 1)^{3rNc} \exp(\frac{rNc}{\upsilon\ T}) \tag{1.23}$$

where Ω_* describe the number of way to distribute the whole set of *mer* and c is the factor reducing degree of freedom of individual segments.

Since the gran-canonical partition function is related to the pressure that from the relation:

$$p = \kappa_B T(\frac{\partial \ln Z}{\partial V})_T$$

The equation of state, Flory EOS, is:

$$\frac{p\ \upsilon^*}{T} = \frac{\upsilon^{1/3}}{\upsilon^{1/3} - 1} - \frac{1}{\upsilon\ T} \tag{1.24}$$

where the macroscopic variables used are dimensionless and υ represents the segment volume.

1.1.4 Guggenheim solution theory

Guggenheim, in his mirable work [23], had given the definition of *surface contacts* of polymer molecule, that is the number of interactions a molecule can done through non specific bonds. The total number of lattice point is given by:

$$N_r = N_0 + \sum_{i=1}^{k} r_i N_i$$

where the *surface* contacts number of n-th polymer molecule, q, defined by the equation [45]

$$qz = (r-2)\cdot(z-2) + 2(z-1) \tag{1.25}$$

$$N_q \equiv N_0 + \sum_{i=1}^{k} q_i N_i$$

$$= N_0 + \sum_{i=1}^{k} \frac{(zr - 2z - 2r + 4 + 2z - 2)}{z} N_i$$

$$= N_0 + \sum_{i=1}^{k} \frac{(r_i \cdot (z-2) + 2)}{z} N_i$$

$$= N_0 + \sum_{i=1}^{k} (r_i \cdot (1 - \frac{2}{z}) + \frac{2}{z}) N_i$$

Then, he gives two main models for the configurations explored by the system. One for the random distribution of sites among the lattice:

$$\Omega = \prod_{i=1}^{k} [\frac{\delta_i}{\sigma}]^{N_i} \cdot \frac{N_r!}{\prod_{i=0}^{k} N_i!} \cdot [\frac{N_q!}{N_r!}]^{(\frac{z}{2})} \tag{1.26}$$

The formula for the non randomness distribution of external contacts is then calculated also. The non covalent bonds formed on the polymer molecule surface are treated as chemical bonds form in a random way. His model is known as *quasi-chemical approximation* The number of configurations, therefore, is well described by:

$$\Omega_{NR} = \frac{N_{rr}^0! N_{00}^0! \left[\frac{N_{r0}^0}{2}!\right]^2}{N_{rr}! N_{00}! \left[\frac{N_{r0}}{2}!\right]^2} \tag{1.27}$$

1.1.5 Solution theory of Sanchez-Lacombe

A molecular theory of classical fluid, based on the Huggins formulations of a fluid on lattice is formulated by Isaac C. Sanchez and by Robert H. Lacombe [28]. Since the model fluid reduces to the classical lattice gas in one special case, it can be best characterized as an Ising or lattice fluid. The model fluid undergoes a liquid-vapor transition. The Ising fluid better correlates experimental saturated vapor pressures and liquid-vapor densities than the van der Waals or related theories. When applied to polymeric liquids it correlates experimental density data as well as less tractable equations derived from cell theories. This theory aim to describe mixtures is very similar to the Flory-Huggins one and the most difference reside in its capability to describe vacations in the lattice such as is capable of describe free volume. Its behaviors is function of pure fluid parameters and can be calculated easily as for liquid as for gaseous phases.

In statistical mechanics the Gibbs free energy, G, is related to the configurational partition function Z in the pressure ensemble by

$$G = -\kappa T ln Z(T, P) \tag{1.28}$$

$$Z(T, P) = \sum_{V} \sum_{E} \Omega(E, V, N) \exp^{-\beta(E+PV)} \tag{1.29}$$

where $\Omega(E,V,N)$ is the number of configurations available to the system of N molecules whose configurational energy and volume are E and V, respectively. The summation extend over all the values of E and V. The properties of derived from the pressure ensemble and the Gibbs potential are identical with those of the more commonly used canonical and gran-canonical ensembles.

The problem is to determine the number of configurations available to the system of N molecules each of which occupies r sites and the N_0 vacant lattice sites, *holes*. This problem as outlined, is still to solve for real models, although an approximate value of Ω for a multicomponent mixture of polymer on a lattice is given by Guggenheim [45]. The Guggenheim solution, for a binary mixture of *r-mers* and monomer like holes, is used to evaluate the partition function 1.29 in the *mean-field approximation*. Starting from the Guggenheim equation 1.26

$$\Omega = \prod_{i=1}^{k} [\frac{\delta_i}{\sigma}]^{N_i} \cdot \frac{N_r!}{\prod_{i=0}^{k} N_i!} \cdot [\frac{N_q!}{N_r!}]^{(\frac{z}{2})} \tag{1.30}$$

then with the application of Stirling approximation of factorial

$$\Omega \simeq \prod_{i=1}^{k} [\frac{\delta_i}{\sigma}]^{N_i} \cdot (\frac{N_r}{e})^{N_r} \cdot \prod_{i=0}^{k} (\frac{N_i}{e})^{-N_i} \cdot [(\frac{N_q}{e})^{N_q} \cdot (\frac{N_r}{e})^{-N_r}]^{(\frac{z}{2})}$$

As we have to deal with the condition

$$N_q = N_0 + \sum_{i=1}^{k} (r_i \cdot (1 - \frac{2}{z}) + \frac{2}{z}) N_i$$

and in the *Flory approximation* (limit of $z \Rightarrow \infty$)

$$\lim_{z \Rightarrow \infty} [N_0 + \sum_{i=1}^{k} (r_i \cdot (1 - \frac{2}{z}) + \frac{2}{z}) N_i] = N_0 + \sum_{i=1}^{k} r_i N_i \Longrightarrow N_q = N_r$$

we get:

$$\begin{aligned}
\Omega = \prod_{i=1}^{k} [\frac{\delta_i}{\sigma}]^{N_i} \cdot \prod_{i=0}^{k} (\frac{N_i}{e})^{-N_i} \cdot (\frac{N_r}{e})^{N_r} \cdot (\frac{N_r}{e})^{(z \cdot \frac{(N_0 + \sum_{i=1}^{k} r_i N_i)}{2})} \cdot (\frac{N_r}{e})^{(-z \cdot \frac{(N_0 + \sum_{i=1}^{k} r_i N_i)}{2})} \\
= \prod_{i=1}^{k} [\frac{\delta_i}{\sigma}]^{N_i} \cdot \prod_{i=0}^{k} (\frac{N_i}{e})^{-N_i} \cdot (\frac{N_r}{e})^{N_r} \\
= (\frac{e}{N_0})^{N_0} \cdot \prod_{i=1}^{k} [\frac{\delta_i}{\sigma}]^{N_i} \cdot \prod_{i=1}^{k} (\frac{N_i}{e})^{-N_i} \cdot (\frac{N_r}{e})^{N_r} \\
= (\frac{e}{N_0})^{N_0} \cdot \prod_{i=1}^{k} [\frac{\delta_i \cdot e}{\sigma \cdot N_i}]^{N_i} \cdot (\frac{N_r}{e})^{N_r} \\
= (\frac{e}{N_0})^{N_0} \cdot \prod_{i=1}^{k} [\frac{\delta_i \cdot e}{\sigma \cdot N_i}]^{N_i} \cdot (\frac{N_r}{e})^{N_0 + \sum_{i=1}^{k} r_i N_i} \\
= (\frac{N_r}{N_0})^{N_0} \cdot \prod_{i=1}^{k} [\frac{\delta_i \cdot e}{\sigma \cdot N_i}]^{N_i} \cdot (\frac{N_r}{e})^{\sum_{i=1}^{k} r_i N_i}
\end{aligned}$$

$$\Omega = (\frac{N_r}{N_0})^{N_0} \cdot \prod_{i=1}^{k} [\frac{\delta_i}{\sigma \cdot e^{r_i - 1}} \cdot (\frac{N_r^{r_i}}{N_i})]^{N_i}. \tag{1.31}$$

The energy of the lattice depends only on nearest neighbor interactions. Furthermore, if it is assumed that the variation of in the interaction energy of an empty site with one containing a molecule, or even empty it, is zero, and assuming random mixing of the sites, Emph approximation of Bragg and Williams also called mean-field approximation, you can define the lattice energy

$$E = -N_r \sum_i \sum_j f_i \cdot f_j \cdot \epsilon_{i,j}^* \tag{1.32}$$

where $\epsilon_{i,j}^*$ is the average interaction energy of a pair segments and defined as

$$\epsilon_{i,j}^* \equiv (\frac{z}{2}) \cdot \epsilon_{i,j}$$

f_i is the occupation fraction of lattice sites of type i.

The close packed volume of an N r-mers system is

$$V^* = N \cdot (r \cdot v^*) \tag{1.33}$$

where the following equations hold

$$r = \sum_i \chi_i r_i \quad \chi_i = \frac{N_i}{N} \quad N = \sum N_i.$$

The total volume of the mixture is

$$V = N_r \cdot v^*$$

with v^*, cell volume, calculated using the relation

$$r \cdot v* = \frac{M}{p*}$$

where p * is the crystallographic density and M the molecular weight. The number of pair interactions is supposed to be the same as the fluid constructed with only one component $(z/2)$ rN.

In the gas system of the large Gibbs partition function it is supposed:

$$Z(T,P) = \sum_{N_0}^{\infty} \Omega \exp\left(-\beta(E + PV)\right). \tag{1.34}$$

Since $G = -\kappa_B T \; lnZ$ is permissible to write

$$\tilde{G} = -\tilde{\rho} + \tilde{P}\tilde{v} + \tilde{T}(\tilde{v} - 1)$$
$$\cdot \ln(1 - \tilde{\rho} + \frac{1}{r} \ln \rho + \sum \frac{\phi_i}{r_i} \ln(\frac{\phi_i}{\Omega_i})).$$

The definition of reduced thermodynamic variables are:

$$\tilde{P} = \frac{P}{P^*} = P \cdot (\frac{\nu^*}{\epsilon^*}); \tag{1.35}$$

$$\tilde{T} = \frac{T}{T^*} = T \cdot \frac{R}{\epsilon^*} = T \cdot (\frac{N_A \cdot k_b}{\epsilon^*}); \tag{1.36}$$

$$\tilde{\rho} = \frac{1}{\tilde{v}} = \frac{V^*}{V} = \frac{(r \cdot N_r \cdot \nu^*)}{V}, \tag{1.37}$$

where P_* is the characteristic pressure, T_* is the characteristic temperature, r is the number of segment molecule can be divided, N_r is the number of lattice fluid cell occupied by polymer and , ν^* stay for closed packed cell volume as

$$\nu^* = \frac{V^*}{N_r \cdot r}$$

.

Minimizing the energy function of the number of empty cells or equivalently as a function of the reduced volume $\tilde{v}$, through

$$\frac{\partial G}{\partial \upsilon} = 0$$

brings to the equation of state:

$$\tilde{\rho}^2 + \tilde{P} + \tilde{T}[\ln(1-\tilde{\rho}) + (\frac{r-1}{r})\tilde{\rho}] = 0. \tag{1.38}$$

The equation can also be obtained using the classical equation

$$V = \frac{\partial G}{\partial P}_T$$

The model fluid undergoes a liquid-vapor transition. Only three molecular parameters are required to describe a fluid; these parameters have been determined and tabulated for several fluids. Although they can easily obtained for the pure component by fitting their physical properties with the model equations. The molecular weight dependence of the critical point and boiling point of a homologous series of fluids such as the normal alkanes is correctly predicted. The equation of state does not satisfy a simple corresponding states principle, although polymeric liquids of sufficiently high molecular weight do satisfy a corresponding states principle. The Ising fluid better correlates experimental saturated vapor pressures and liquid-vapor densities than the van der Waals or related theories. When applied to polymeric liquids it correlates experimental density data as well as less tractable equations derived from cell theories. The basic simplicity and structure of the theory readily suggests a easy use in technological mixtures, when the molecular parameters are completely characterized for pure fluid. In the case of mixtures, similar reduced variables are introduced, but the scaling variables are averaged of their corresponding values of pure components calculated by proper mixing rules. It is evident that, since this model does not assume volume additivity, as opposed to Flory-Huggins theory, it is intrinsically better suited to describe the behavior of systems in which significant change in the volume are associated to the formation of the mixture. This model can predict the existence of a lower critical solution temperature, LCST, where demixing of the mixtures occur as temperature is raised.

1.1.6 Staverman non-covalent contact number

Huggins theory have to be extended to include polymer molecules and not, having rings or cross-link. Staverman clearly exposed [45] a new definition of q as *non-bonded* contact number in the lattice. This latter is of not easily determination, however is upper limited by Guggenheim relation [23].

$$q \cdot z = r \cdot z - 2 \cdot r + 2$$

The equation describe the number of non covalent contacts owned by a long linear polymeric molecule in a lattice fluid model. Note that the value calculated by this equation are the number of non-covalent bonds inclusive of the bonds between the sub-units of the same molecule, between different molecules and covalent bonds, rings and cross-link.

Staverman gives a generalized expression for the configurational term, Ω.

$$\Omega = \omega^N \frac{N_r! N_r^{lN}}{N_0! N!} \cdot \left[\frac{N_q!}{N_r!}\right]^{\left(\frac{z}{2}\right)} \tag{1.39}$$

where

$$l = \frac{z}{2} \cdot (r - q) - (r - 1)$$

$$qz = (r - 2) \cdot (z - 2) + 2(z - 1).$$

1.1.7 The hydrogen bond bridge in fluids

The hydrogen bond has always been a subject of interest in all fields of science. Its peculiarities and its importance in various fields such as protein folding, in their functionality, in changing the properties of emulsions and in general the solutions made it the most important link after the strictly chemical. When assessing the environmental durability of a polymer matrix, the account for specific polymer-solvent interactions is needed. In fact many penetrants, including water molecules, can profoundly affect polymer structure by establishing strong interactions, which can disrupt the structure of the matrix. The stabilization energy of the hydrogen bond, which is given vary between 2 and 30 kcal / mol, it makes it a fairly strong and stable bond, important in determining the structural conformations of polymers they both natural and synthetic. The thermally induced phase separation phenomena in the mixtures (LCST) find their theoretical explanations both in compressibility over that in the specific interactions between components. Well known is that the LCST behavior resulting from the finite compressibility is described approach equation of state. Little is known about the specific interactions and their importance in describing the thermodynamic behavior of mixtures with a preponderance of hydrogen bridge interactions. However, all the approaches described above are well suited only for systems that do not display specific interactions since, in the case of LF-EoS only a *mean field contribution* is considered when constructing the expression of the Gibbs free energy.

1.1.8 The NRHB equation of state

In *Non Random Hydrogen Bond* model hydrogen bonding interactions are calculated explicity. Lattice Fluid theories have been further developed to include

the effect of the possible self- and cross-interactions in polymer-penetrant systems. In particular, Panayiotou and Sanchez [12] have modified the original Sanchez Lacombe *lattice fluid*-EoS theory to include the formation of specific interactions, that is, Hydrogen-Bonding in mixtures. The equation of state here showed is valid for systems with hydrogen bonds both in the liquid state and gaseous, like other EOS theories. In a molecular system, nonidealities appear as a result of the nonrandom distribution of molecular segments in the lattice as well as specific interactions between neighboring *mer*, such as hydrogen bonds. Therefore the Sanchez Lacombe theory, also called SL, was further modified to include the effect of nonrandomness contribution as to *mean field* interactions as to specific interactions. Thus, the intermolecular forces are considered to be divided into two types: those of non-specific interaction of Van Der Waals forces and those specific, but the canonical partition function is then considered to be factorized into three canonical partition functions describing a nonspecific physical interactions with randoms distribution of segments, one for the nonrandom distribution and the last one for the binding interactions due to hydrogen bonds.

$$Z = Z_R Z_{NR} Z_{HB} \tag{1.40}$$

Accurate expression for this terms was, over the years, proposed by Panayitou and co-workers, resulting in different variations of the theory.

In the first model, the configurational energy of the system is divided in polar and non-polar term, in the assumption that the number of configuration explored by the system can be factorized as energy term. This is non the real and this method calculating an integral beside much used is clearly an approximation.

It is worth noting that the *mean field* lattice fluid theory described above, both the original ones and those modified to account for specific interactions, are based on a simplified statistical framework in which the arrangement of *r-mers* and holes is assumed to be at random. However, in the case of non regular contacts between different kinds of *r-mers* such assumption is likely to be incorrect. On the basis of the pioneering work of Guggenheim [45], several theories have been developed to deal with the non-randomness distribution of contacts in lattice fluid, first tackling the cases in which occurrence of specific interactions is non accounted for. In this model, in spite of first models developed, non randomness of contacts between mers of various components and holes generally is assumed. Resulting in the two first terms in equations 1.40. This approach is, in the time, fully extended to specific hydrogen bonds by the contribution of Panayiotou and Yeom [37], but this model describe the nonrandom distribution of specific bonds over the lattice in the second term of equation 1.40. In the following we refer to this theory as *non random Hydrogen Bonding*, NRHB. The model is based on a compressible lattice theory and accounts for the non-randomness of lattice fluid contacts and possible formation of hydrogen bonds.

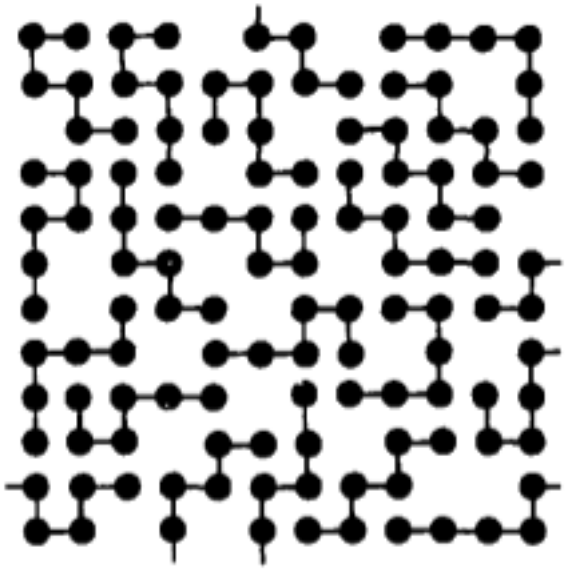

Figure 1.2: Segments of a chain polymer molecule located in the liquid lattice with holes

Let us consider a system of N_i molecules of a component i, at temperature T and an external pressure P. Let each componet of t types, assumed to be arranged in a semi-crystalline way with coordination number z and of N_r sites, of which N_0 are the empty sites. The number of molecules in the lattice, N, is given by

$$N = \sum_{i}^{t} N_i.$$

Each molecule is assumed to be divided in r_i segments, or *mers*, of individual volume of ν_i^*. The total number of sites is given by:

$$N_r = N_0 + \sum_{i}^{t} r_i \cdot N_i = N_0 + \sum_{i}^{t} \chi_i r_i N \tag{1.41}$$

where χ_i are the molar fractions of the component i, as defined by

$$\chi_i = \frac{N_i}{N}.$$

The average interaction energy in the *mean field approximation* is given by

$$\epsilon_i^* = \frac{z}{2}\epsilon_{ii} \tag{1.42}$$

where ϵ_{ii} is the interaction energy for a *mer mer* contacts of the component i.

If the number of external contacts per molecule is zq, can be defined a surface to volume ratio, s, as a geometric constant for each molecular type and is given by:

$$s_i = \frac{q_i}{r_i} \tag{1.43}$$

In a mixture, parameters r and q are simply calculated through the following mixing rules:

$$r = \sum_i^t \chi_i r_i \tag{1.44}$$

$$q = \sum_i^t \chi_i q_i \tag{1.45}$$

and so

$$s = \frac{q}{r} \tag{1.46}$$

Furthermore, segmet fractions, ϕ_i and surface fractions, θ_i have to be defined as

$$\phi_i = \frac{r_i N_i}{\sum_k^t r_k N_k} \tag{1.47}$$

and

$$\theta_i = \frac{q_i N_i}{\sum_k^t q_k N_k} = \frac{\phi_i s_i}{s} \tag{1.48}$$

The total number of contact site in the system is

$$zN_q = zqN + zN_0 \tag{1.49}$$

while the total volume of the system is given by the expression

$$V = Nr\nu^* + N_0\nu^* = N_r\nu^* = V^* + N_0\nu^* = V^*\tilde{\nu} \tag{1.50}$$

where the same averaged segmental volume, ν^* is assigned to an empty site and to the occupied ones. ν_* is assumend to be constant among all fluids and is set equal to 9.75 $cm^3 mol_{-1}$. To be note that V^* is the total closed packed volume.

In order to incorporate the non-randomness in the distribution of the contacts in the system, we will assume that the partition function of the system, in the isothermal-isobaric statistical ensemble can be factorized as follow:

$$Z(N, P, T) = \Omega_R \Omega_{NR} exp^{-\frac{E+PV}{RT}} \tag{1.51}$$

where Ω_R is the number of configurations available for a hypothetical system with a fully random distribution of holes and Ω_{NR} is the correction of the previous number of configurations that accounts for the non-randomness of the empty sites.

For the first combinatorial factor, we will adopt the generalized expression of Staverman 1.39, modified for the mixture model:

$$\Omega_R = \prod_i^t \omega_i^{N_i} \frac{N_r! \prod_i^t N_r^{l_i N_i}}{N_0! \prod_i^t N_i!} \cdot \left[\frac{N_q!}{N_r!}\right]^{(\frac{z}{2})} \tag{1.52}$$

where ω_i is a characteristic quantity for each fluid that takes into account the flexibility and symmetry of the molecule i. For the calculations of interest this term cancel itself out. The parameter l, in equation 1.52 is equal to:

$$l = \frac{z}{2}(r-q) - (r-1)$$

For the second factor we will use the Guggenheim expression for the *quasi-chemical* theory, as proposed in the original model:[23]

$$\Omega_{NR} = \frac{N_{rr}^0! N_{00}^0! \left[\frac{N_{r0}^0}{2}!\right]^2}{N_{rr}! N_{00}! \left[\frac{N_{r0}}{2}!\right]^2} \tag{1.53}$$

In this equation, N_{rr} is the number of external contacts between the segments belonging to molecules, N_{00} is the number of contacts between empty sites, and N_{r0} is the number of contacts between a molecular segment and an empty site. The superscript 0 refers to the case of randomly distributed empty sites. Therefore, in the random case N_{rr} equation takes the form:

$$N_{rr}^0 = \frac{1}{2} zqN \frac{qN}{N_0 + qN} = \frac{z}{2} qN\theta_r \tag{1.54}$$

where θ_r is given by:

$$\theta_r = 1 - \theta_0 = \frac{q/r}{q/r + \tilde{v} - 1}$$

and the reduced volume is:

$$\tilde{v} = \frac{V}{V^*} = \frac{1}{\tilde{\rho}} = \frac{1}{\sum_i^t f_i}$$

where $\tilde{\rho}$ is the reduced density and f_i is the site fraction of the component i, and its relation to the holes site fraction is related by the equation:

$$f_0 = \frac{N_0}{N_r} = \frac{N_r - \sum_i^t r_i N_i}{n_r} = 1 - \sum_i^t f_i \tag{1.55}$$

In the random case the number of contacts between a segment and an empty site is given by

$$N_{r0}^0 = zqN \frac{N_0}{N_q} = zN_0 \frac{qN}{N_q} = zN_0\theta_r, \tag{1.56}$$

while the number of contacts between empty sites is:

$$N_{00}^0 = \frac{1}{2} N_0 z \frac{N_0}{N_q} = \frac{z}{2} N_0\theta_0, \tag{1.57}$$

and the number of contacts between *mers* is

$$N_{rr}^0 = \frac{z}{2N_q} \left(\sum_i^t (q_i N_i)^2 \right) + \frac{z}{N_q} \sum_i^t \sum_{j>i}^t q_i N_i q_j N_j \tag{1.58}$$

The number of nonrandom inter-segmental contacts will be obtained by *quasi chemical* theory,following the equations:

$$N_{ii} = N_{ii}^0 \Gamma_{ii}$$
$$N_{ij} = N_{ij}^0 \Gamma_{ij}$$
$$N_{00} = N_{00}^0 \Gamma_{00}$$
$$N_{i0} = N_{i0}^0 \Gamma_{i0}$$

The non-random Γ factors in this equation must satisfy the following balance relations:

$$\sum_{j>i}^{t} \sum_{i=0}^{t} \theta_i \Gamma_{ij} = 1 \tag{1.59}$$

In this model we assume that only the first-neighbor segment-segment interaction contacts contribute to the potential energy and, thus, we may write:

$$-E = \sum_{i=1}^{t} N_{ii} \epsilon_{ii} + \sum_{i=1}^{t} \sum_{j>i}^{t} N_{ij} \epsilon_{ij} \tag{1.60}$$

and

$$\epsilon_{ij} = \sqrt{\epsilon_{ii} \epsilon_{jj}} \, (1 - k_{ij}) \tag{1.61}$$

where k_{ij} is a binary interaction parameter between species i and j and is fitted to binary experimental data, as we see below.

Then the Gibbs free energy of the system is obtained from the partition function in the pressure ensemble and from statistical thermodynamics as follow:

$$G = -RT \ln Z(N,P,T) \tag{1.62}$$

The reduced density at equilibrium is obtained from the free energy minimization that occurs from:

$$\left(\frac{\partial G}{\partial \tilde{\rho}} \right)_{T,P,N,N_{ro}} = 0 \tag{1.63}$$

while the non-trandom number of contacts, N_{r0}, is obtained by minization of free energy versus this number itself, such as in condition:

$$\left(\frac{\partial G}{\partial N_{r0}} \right)_{T,P,N,\tilde{\rho}} = 0 \tag{1.64}$$

Combining the equation 1.63 with 1.51,1.52 and 1.53 we have:

$$\tilde{P} + \tilde{T} \left[\ln(1 - \tilde{\rho}) - \tilde{\rho} \cdot [\sum_{i}^{t} \phi_i \frac{l_i}{r_i}] \right] + \\ - \tilde{T} \left[\frac{z}{2} ln[1 - \tilde{\rho} + \frac{q}{r} \tilde{\rho}] + \frac{z}{2} ln \Gamma_{00} \right] = 0 \tag{1.65}$$

The scaling temperature T^* and pressure P^* are established relating theirself to the mean field interaction energy, ϵ^* by the relation:

$$\epsilon^* = RT^* = P^* v^* \tag{1.66}$$

$$\epsilon^* = \sum_{i=1}^{t} \sum_{j=1}^{t} \theta_i \theta_j \epsilon_{ij}^* \tag{1.67}$$

where ϵ_{ij} is defined by the equation 1.61.

The reduced temperature and pressure are defined as:

$$\tilde{T} = \frac{T}{T^*} = \frac{RT}{\epsilon^*}; \tag{1.68}$$

$$\tilde{P} = \frac{P}{P^*} = \frac{P\nu^*}{RT^*}. \tag{1.69}$$

The *nonrandom* factors, Γ_{ij}, are calculated by the $t(t+1)/2$ equations:

$$\frac{\Gamma_{ii}\Gamma_{jj}}{\Gamma_{ij}^2} = \exp^{\frac{\Delta\epsilon_{ij}}{RT}} \tag{1.70}$$

also known as *quasi chemical* conditions where

$$\Delta\epsilon_{ij} = \epsilon_{ii} + \epsilon_{jj} - 2\left(1 - k_{ij}\right)\sqrt{\epsilon_{ii}\epsilon_{jj}} \tag{1.71}$$

The equation 1.70 and 1.59 constitute a set of non linear algebraic equations which should numerically solved for mixtures in order to obtain the nonrandom factors.

For phase equilibrium calculations, the property of equivalence of the chemical pontential of the two phase have to be used.

$$\mu_1 = \mu_2 \tag{1.72}$$

The chemical potential obtained from the equation 1.64 have the following equation:

$$\begin{aligned}\frac{\mu_i}{RT} = \ln\frac{\phi_i}{\omega_i r_i} - r_i \sum_j^t \frac{\phi_j l_j}{r_j} + \ln\tilde{\rho} + r_i(\tilde{\nu}-1)\ln\left[1-\tilde{\rho}\right] + \\ - r_i\frac{z}{2}\left[\tilde{\nu} - 1 + \frac{q_i}{r_i}\right]\ln\left[1 - \tilde{\rho} + \frac{q}{r}\tilde{\rho}\right] + \\ + \frac{zq_i}{2}\left[\ln\Gamma_{ii} + \frac{r_i}{q_i}(\tilde{\nu}-1)\ln\Gamma_{00}\right] - \frac{q_i}{\tilde{T}} + r_i \cdot \frac{\tilde{P}\tilde{\nu}}{\tilde{T}}\end{aligned} \tag{1.73}$$

The equations presented are sufficient for solving phase equilibrium and calculating basic thermodynamics quantities of pure fluid of any molecular size. When the fluid interact with hydrogen bonds, the above equations must be changed as show in next paragraph.

Hydrogen Bonding Following the work of Panayioutou [12, 27], it will be assumed here that the intermolecular forces may be divided into physical and chemical (or hydrogen bonding). The direct implication of this is that the partition fuction consist of two contributions: one physical, obtained from expressions of the previous paragraph and one chemical or hydrogen bonding, which will be denoted by subscript HB. Furthermore, using equation 1.62 we can, through the standard thermodynamic equations, the hydrogen bond contribution to Gibbs free energy, chemical potential, enthalpy and so forth can be calculated. We consider that there are m types of proton donors and n types of proton acceptors in the system. Let d_i be the number of donor groups of type i in each molecule and a_j be the number of acceptor groups of type j in each molecule. Let $N_{ij,HB}$ be the total number of hydrogen bonds between a donor of type i and an acceptor of type j in the system. Using the lattice fluid procedure, reported in the previous section, we obtain for the equation of state of the fluid

$$\tilde{P} + \tilde{T}\left[\ln(1-\tilde{\rho}) - \tilde{\rho}\cdot\left(\sum_i^t \phi_i \frac{l_i}{r_i} - \nu_H\right)\right] + \\ - \tilde{T}\frac{z}{2} ln\left[1 - \tilde{\rho} + \frac{q}{r}\tilde{\rho}\right] + + \tilde{T}\frac{z}{2} ln\Gamma_{00} = 0 \quad (1.74)$$

with ν_H being the hydrogen bonding contact number following the formula:

$$\nu_H = \sum_\alpha^m \sum_\beta^n \nu_{\alpha\beta} = \sum_\alpha^m \sum_\beta^n \frac{N_{\alpha\beta}}{rN}. \quad (1.75)$$

The full expression of the chemical potential of component i in the mixture is calculated by adding to equation 1.73 the following hydrogen bond contribution:

$$\frac{\mu_{i,HB}}{RT} = r_i \nu_H - \sum_{\alpha=1}^m d_\alpha^i ln \frac{\nu_d^\alpha}{\nu_{\alpha 0}} - \sum_{\beta=1}^n a_\beta^i ln \frac{\nu_a^\beta}{\nu_{\beta 0}} \quad (1.76)$$

where

$$\nu_d^\alpha = \frac{N_d^\alpha}{rN} = \frac{\sum_k^m d_\alpha^k N_k}{rN} \quad (1.77)$$

and

$$\nu_a^\beta = \frac{N_a^\beta}{rN} = \frac{\sum_k^n a_\beta^k N_k}{rN} \quad (1.78)$$

while

$$\nu_{\alpha 0} = \nu_d^\alpha - \sum_\beta^n \nu_{\alpha\beta} \quad (1.79)$$

and similiar

$$\nu_{\beta 0} = \nu_a^\beta - \sum_\alpha^m \nu_{\alpha\beta} \quad (1.80)$$

Then we minimize the number of hydrogen bond contact minimizing, for all hydrogen acceptor and donor group, the reported condition:

$$\frac{\nu_{\alpha\beta}}{\nu_{\alpha 0}\nu_{0\beta}} = \tilde{\rho}\exp^{-\frac{G^H_{\alpha\beta}}{RT}} \quad (1.81)$$

where

$$G^H_{\alpha\beta} = G^H_{\alpha\beta} + PV^H_{\alpha\beta} - TS_{\alpha\beta}.$$

Here $G^0_{\alpha\beta}$,$E^0_{\alpha\beta}$,$S^0_{\alpha\beta}$ and $V^0_{\alpha\beta}$ represent,respectively, the molar Gibbs energy of formation, the molar internal energy of formation, the molar entropy of formation and the molar volume of formation associated to hydrogen bonding between the proton donor group of type α and the proton acceptor group of type β.

The molecular parameters In the formulation of the NRHB model, for every fluid parameters are required. For pure fluid, as in the previous theory developed by Sanchez and Lacombe, three parameters are needed for the non specific interactions. That are: the self segment interaction energy, ϵ^*; the segmental volume, ν^* and the closed packed segmental specific volume, ν^*_{sp}. As already mentioned, in this model the segmental volume is considered constant over a wide range of fluids and conditions. Furthermore, the interactional energy and volume clsed packed for segment are linearly expanded over temperature by relations:

$$\epsilon^* = \epsilon^*_H + (T - 298.15)\,\epsilon^*_s; \tag{1.82}$$

$$\nu^*_{sp} = \nu^*_{sp,0} + (T - 298.15)\,\nu^*_{sp,1}. \tag{1.83}$$

The subscript, in the equation 1.82, h and s denote an *enthalpic* and *entropic* contribution to the energy. The volume constant $\nu_{vp,1}$ is assumed to have a constant value over class of fluids.

Therefore, only three adjustable parameters are needed for the calculations of pure fluids without any hydrogen bond capabilities, which are: ϵ^*_h,ϵ^*_s and $\nu^*_{sp,0}$. These parameters are fitted to the experimental saturated liquid density and vapour pressure of pure components.

For hydrogen bonding fluids, the theory needs an additional three parameters for pure fluids which are the energy E^H_i, the volume, V^H_i and the entropy variations, S^H_i, involved in the formation of a self hydrogen bond interaction. Three others are needed for any additional hydrogen bonds interactions.

Chapter 2

Computational methods

2.1 Introduction

The large majority of molecular problem of practical interest, today, are unfortunately too large to be described by *quantum mechanics*. Quantum mechanical simulations, classically, deal with all the electron of system making this kind of approach unsuitable with as polymer solutions as biological system, cause of their big size model describing the quantum mechanical behavior of these systems are too much time consuming and well defined models can only be found in unreachable future. Molecular mechanics instead ignores the electronic behavior and their motions. Calculate the energy can be done more easily than quantum mechanics as it was function of sole nuclear coordinates. Thus, it is the best choice that can be done in order to be time-saving and to perform calculations on very large system, thus containing a very large number of atoms. Although, this way seems to be likely, the lack of informations on electron's distribution on molecule and the possibility to change their distributions over different atoms brought difficulties in the insight to deal with specific interactions in the model.

2.2 Molecular mechanics: basic principle

In order to analyze any reaction, the main goal to achieve is to have the potential energy surface calculating the electronic energy for a given nuclear configuration. In *molecular mechanics* (MM) methods this step is bypassed by averaging the electronic energy as a function of nuclear parameters, such as nuclear charge, mass and electronic configuration. These functions are found fitting experimental or higher level calculations. The only particle in molecular mechanics calculations are atoms, none electron is considered as individual particle. To be note their bound energy between atoms cannot found *ab-initio* but should be provided through other methods rather being the result of solving electronic Schroedinger equation. The nuclei quantum aspects of their motions are to be neglected too in this formulation. The foundation of molecular mechanics is the observation that molecules tend be composed of units that are structurally similar as stated by *Atom In Molecule* (AIM) quantum theory. All the energies and lengths of a kind of chemical bond tend to be roughly constant. Therefore molecules are wholly treated by classical mechanics and as *ball and string*

model, their laws of motion are entirely described by their coordinates and force field.

$$\frac{d^2\chi_i}{dt^2} = \frac{F_i}{m_i} \tag{2.1}$$

Then their time evolutions, potential energy surface can be entirely explored, due to Newton's laws and classical mechanics laws. In molecular dynamics successive configurations of the system are generated by integrating Newton's law of motion. Molecular mechanics models are also referred to as *force field* (FF) methods.

2.2.1 Force field energy

To be deal with molecular mechanics the first step is to define a force field. In general expressed in terms of an interaction potential.

$$F_{\chi_i} = \frac{\partial V}{\partial \chi_i} \tag{2.2}$$

Interaction can be broken up into terms involving each interaction between pairs, triplets and so on.

$$V = \sum_i v_1(r_i) + \sum_i \sum_{j>i} v_2(r_i, r_j) + \\ + \sum_i \sum_{j>i} \sum_{k>j>i} v_3(r_i, r_j, r_k) + ... \tag{2.3}$$

In molecular mechanics, the energy of the system can be calculated as the summation of term each one involving the energy variation required to distorting a molecule in a specific fashion.

$$E_{MM} = E_{str} + E_{bend} + E_{tors} + E_{vdw} + E_{el} + E_{cross} \tag{2.4}$$

E_{str} is the energy function describing *stretching* of a bond between two atoms. E_{bend} represents the energy variation involved in *bending* of a angle formed by three atoms, $E_{torsion}$ is the energy for rotate the system around a bond between two atoms, E_{vdw} and E_{el} terms describe the *non-bonded* energy due to atom-atom interactions,

Given such an energy function of the nuclear coordinates, geometries and relative energies can be found by calculations as the stable ones correspond to relative minimum in potential energy surface. Thus stationary coordinates of nuclei in a molecule can be found minimizing the energy as a function of their internal coordinates.

The stretch energy Bonding energy regards every system arranged in molecular structures, it is related to the stiffnes of a chemical bond. In principle the molecular systems could be treated as like as atomic systems. Chemical bonds are in fact likely inter atomic potential energy term involving two atoms coordinates. Obviously, to deal with chemical bonding and with chemical reactions means to deal with quantum mechanics. The use of a this classical approximation would in fact causes serious errors and could not predict any

chemical reaction that occurs through the disruption and/or creation of a covalent bond. Although, molecule can be treat as rigid or semi-rigid units with bond length, bond angle and torsional angle fixed or oscillating around equilibrium values. This stand on the consideration that bond vibrations are of very hight frequency but of low amplitude (therefore of no practical importance at room temperature). Figure 2.2.1 show the energy curve for a typical bond.

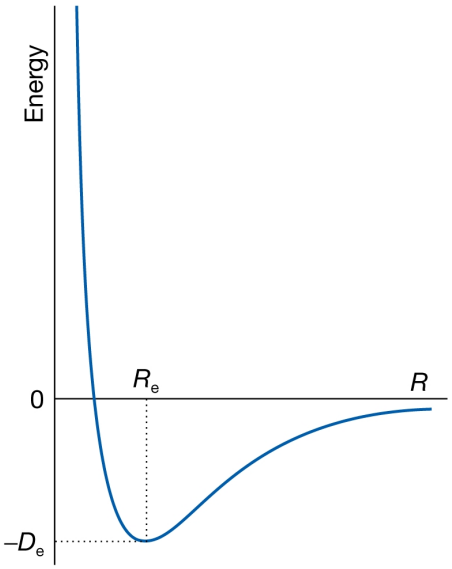

Figure 2.2.1: Represents the morse potential diagram as function of interatomic distance

One way describing this curve is Morse function. The Morse potential has the following form:

$$E_{Morse}(\Delta R) = D(1 - \exp^{-\alpha \Delta R})^2 \tag{2.5}$$

where:

$$\alpha = \sqrt{\frac{k}{2D}}.$$

The Morse potential is non used in force field theories cause it is not amenable to efficient computation as because it required three parameters for every bond. Taylor expanding of the potential around energy minimum, until the second order and simplifying the zero and first order such they are zero at equilibrium, lead to a simplest equation resembling the Hook law.

$$E_{streching}(\Delta R) = k^{AB}(\Delta R^{AB})^2 \tag{2.6}$$

Hooke's law functional form is reasonable approximation of potential curve near the bottom of the potential well.

the bending energy The bending of angle formed of three atoms (A,B,C) involved a functional form that is usually expanded as a Taylor series around a *stationary angle* and terminated to the second order. This derivation lead to the *harmonic approximation* that resemble the Hook's law.

$$E_{bending}(\theta^{ABC} - \theta_0^{ABC}) = k^{ABC}(\theta^{ABC} - \theta_0^{ABC})^2 \tag{2.7}$$

where θ is the angle between the three atoms involved in the potential energy of bending.

This simple expansion is adequate for most of the practical usage although there may be cases where higher accuracy is required. More complex bending potential are available in literature.

The torsional energy The four-bodies interactions discussed represent the hard degree of freedom because the variations of such parameters are much energy demanding. Structural properties due quite entirely to torsional and non-bonded potentials that select the interplaying through conformations of a given system. The form of this potential is periodic, a $2 \cdot \pi$ rotation give us the same functional form. Therefore it can be accurately described as series of periodic function like cosine having frequency as a fraction of $2 \cdot \pi$.

$$E_{tors}(\omega) = \sum_{n=1} V_n cos(n\omega) \tag{2.8}$$

One of the most used popular expression for the functional form is:

$$\begin{aligned} E_{tors}(\omega^{ABCD}) = & \frac{1}{2}V_1^{ABCD}(1 + cos(\omega^{ABCD}))+ \\ & \frac{1}{2}V_2^{ABCD}(1 + 2cos(\omega^{ABCD}))+ \\ & \frac{1}{2}V_3^{ABCD}(1 + 3cos(\omega^{ABCD})). \end{aligned}$$

The *van der Waals* energy Electrostatic interactions cannot account for all of the non-bonded interactions occuring in a system. An obvious example is represented by noble atom gas where, all of the dipole moments are zero and thus there are no electric interactions. Clearly there are some interactions between atoms of the system to justify the condensed behavior. These kind of forces are generally called *van der Waals* forces. They differ from covalent and ionic bonding in that they are caused by correlations in the fluctuating polarizations of nearby particles (a consequence of quantum dynamics).

The best known of van der Waals potential is the Lennard-Jones (also known as 12-6) function, that have the form of the equation reported.

$$v(r) = 4\varepsilon \left[\left(\frac{\sigma}{r}\right)^{12} - \left(\frac{\sigma}{r}\right)^{6} \right] \tag{2.9}$$

where σ is the collision diameter and ε the well depth.

The electrostatic energy Electronegative elements attract electrons more than less electronnegative elements, giving rise to an unequal distribution of charge in a molecule. This charge distribution can be represented in a number of ways, one common approach being an arrangement of fractional point charges through the molecule. The charge are designed to reproduce the elctrostatic properties of molecule. If the charges, as usually done, are restricted to

the nuclear centers they are often referred to as *partial atomic charges*. The potential electrostatic energy between molecules or charge points is the calculated as follow:

$$V = \sum_i \sum_j \frac{q_i q_j}{4\pi\varepsilon_0 r_{ij}} \tag{2.10}$$

The electrostatic properties of a molecule are a consequence of the distribution of the electrons and the nuclei and thus it is reasonable to assume that one should be able to obtain a set of a partial charges using quantum mehcanics. Unfortunately, the partial charge cannot be unambiguosly calculated from the wave-function. This explain the numerous ways to determine partial charges have been proposed. Indirect comparison of the vaious methods are possible, ussually, by calculating appropriate quantities from the charge model and then comparing the results to the experimental. Sometimes model needs a better description of the electric field than the partial charge model, then we use the pseudo atoms charge model, where some new points, carrying only an electric charge, are added to the force field.

2.2.2 Boundary conditions

In molecular mechanics great role have to be devoted to boundary conditions. Then their correct treatment is necessary anyone want to deal with *macroscopic* properties. In real system with typical volume as of practical treatment as liter, the great majority, as 99,99999 ‰, of molecule do not feel the walls of the container. Thus molecular mechanics as molecular dynamics have to deal with number of molecules of the Avogadro number magnitude, it is clearly unfeasible as it require as much time on time on ordinary calculator as the time of the universe. Suitable boundary conditions are therefore adopted to overcame this drawback. We can divide boundary conditions in two groups: periodic boundary conditions and non periodic boundary conditions.

Periodic boundary conditions Periodic boundary conditions are used in the most of applications to simulate real system in which the particle experience force as if they were in the bulk. With this approach we can simulate this behavior we talk about as a much simple system constituted of a small number of particle fashioned in a periodic way. To be clear how to periodic boundary conditions work we can deal with a cubic box.

In figure 2.1 each box is surrounded by 8 box as it is a two dimensional case, in three dimensional model a box have 20 other box surrounding it. If a particle move from its position in the central cell appears as an image particle entering the opposite side of the box as illustrated. Then the number of particle inside the box remain constant in the calculations. In order to easily handle the coordinates of each atom, all calculations are done in the *minimal image* convention. That is, their coordinate are rescaled over the cell parameters and the distance over the neighborhood atoms are done in the appropriate matter as illustrated in Appendix A. This way allow to handle only the atoms in the box and calculates the distance between every atoms in the range of the half cell dimension, as illustrated in Figure 2.2.

Many types of cell can be allowed in this model provided they full cover the entire space as they repeat in any directions.

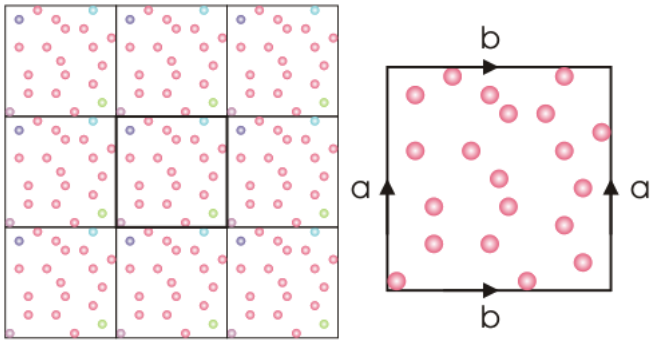

Figure 2.1: Bi-dimensional representation lattice showing periodic conditions

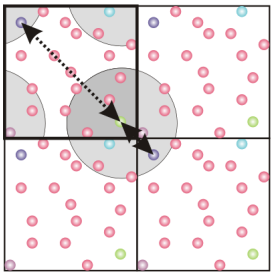

Figure 2.2: Bi-dimensional representation lattice showing minimal image convention

2.3 Molecular dynamics: basic principle

In molecular mechanics we have a very simple Lagrangian description of the model, this allow us in theory to totally describe the time evolution by integrating the Newton's laws of motion.

$$\frac{d^2\chi_i}{dt^2} = \frac{F_{\chi_i}}{m_i} \tag{2.11}$$

Th $v_i \cdot \delta t$ where v_i is the constant velocity and δt_i is the time involved in the integration to time evolution. The case, in which the force acting on each particle depends on the other particle's position, has no easily analytical solution in every case of practical interest in polymers science. Therefore a *numerical calculation* have to be engaged in. In a molecular dynamics simulation, theoretically, we have to consider that the force on each particle will change during time because of the particles positions changes. Finite difference techniques are the most commonly used methods to generate molecular dynamics trajectories with continuos potential models. these techiques are based on the discretization of the motion equation. Molecular dynamics are thus obtained at each δt. More particularly, from the total force on each particle at time t, calculated as the vector sum oft its interactions with other particles, their acceleration at time t is determinated. From the position and velocity at time t we can calculated the position and velocity at the time $t+\delta t$. The process is then iterated to find next system configuration. During each step the force is assumed to be constant.

2.4 Density functional theory

2.4.1 Introduction

Early on in the study of extended periodic systems, it was realized that the wavefunction approach presented by Schroedinger would be rather unsuitable for systems containing many identical and interacting particles. This has prompted the

search for methods that involve fewer variables than the wavefunction and that can be used to calculate the energy and other properties. One approach that has enjoyed a great deal of success is to recast the problem so that the basic variable is the real-space density, $\rho(r)$, a function of only three variables; then the total energy is constructed as a functional of the electrons density. The earliest tractable approach, using this density functional method, was the Thomas-Fermi-Dirac method, which had several failings, such as the inability to bind atoms and form molecules. The most important modern density functional method was developed by Kohn and Sham [38] for which Kohn was awarded the Nobel prize in Chemistry in 1998. This, along with accurate approximations of the exchange-correlation functional, provide the basis for all modern calculations performed with Density Functional Theory (DFT). In the following we will provide a short overview of DFT because all calculations reported in this thesis are based on that theory.

2.4.2 Basics of density functional theory

In quantum mechanics, there is no doubt that the ground state electronic density is determined by the external potential. One of the most important proofs supporting DFT is that this relationship can be inverted, [38] that is, given a ground state density, the potential can be unambiguously recovered.

Hohenberg-Kohn Theorems

The electronic wavefunction of a n-electron molecule depend on $3 \cdot n$ spatial and n spin coordinates, so the wave function of a many electron molecule contains more information than is generally needed; many details of the wavefunction lack direct physical significance. In 1964, Hohenberg and Kohn proved, through their first theorem, that the ground-state molecular energy, wavefunction, and all other physical properties are uniquely determined by the electron probability density $\rho(x, y, z)$, a function of only three variables. [38] Thus, ρ determines V and hence the wavefunction and all properties of the ground state, such as the kinetic energy $T[\rho]$, the potential energy $V[\rho]$, and the total energy $E[\rho]$. This Hohenberg-Kohn theorem is very general. There is no assumption that the particles are Fermions, Bosons, identical particles, or non-interacting. This and Hohenberg and Kohn second principle, the energy density variational principle, legitimizes the use of electron density $\rho(r)$ as basic variable. In fact all properties of the system, including excited state properties, are, in principle, exact functionals of the ground state density. If we happen to know the ground state density, then, in principle, we know the external potential, and so we can, again in principle, solve the many electron Schrödinger equation and know everything about the system. Of course, this is not yet of any practical use, because the crucial point of using DFT is to avoid to deal with the many-electron Schrödinger equation. The internal electronic energy, T, of a system in its ground state can be expressed as $T = E - V_{ext}$ where V_{ext} is the external potential energy, given by

$$V_{ext} = \int \hat{v}_{ext}(r)\rho(r)dr \tag{2.12}$$

Since E and V_{ext} are functionals of the density, it follows that T is also a functional of the density. Supposing we now have an external potential and a ground state density, which may or may not be the ground state density corresponding to that potential, we can define the variational energy, E_{var}, as

$$E_{var}[v_{ext}, \rho] = T[\rho] + \int \hat{v}_{ext}(r)\rho(r)dr \tag{2.13}$$

The true ground state density for v_{ext} is the density that minimize this energy; this is the second part of the Hohenberg-Kohn theorem. [38] However, the search can only include *allowed* densities: those deriving from a legitimate wavefunction (antisymmetric, normalized, corresponding to a particular V_{ext}). In practice this is handled by choosing a particular form of $\rho(r)$, usually that obtained from a single- determinant *wavefunction* (vide infra). We now define $T[\rho]$ as the minimum of the internal electronic energy

$$\langle\psi|\hat{T} + \hat{V}_{ee}|\psi\rangle \tag{2.14}$$

among all electronic wavefunctions corresponding to the density $\rho(r)$. This is the Levy constrained-search [35] definition for the density functional $T_{HK}[\rho]$. At this stage we are not close to a practical method because exact evaluation of $T[\rho]$ would still require solution of the many-body Schrödinger equation. But supposing we have a functional that gives a good approximation to $T + V_{ee}$ and can be evaluated in a practical manner, then a search should lead to a good approximation to the ground state energy and density. This is the fundamental principle upon which all practical DFT calculation are founded.

The Kohn-Sham Method The key idea in modern density functional theory is to replace the interacting problem with a much simpler noninteracting problem while keeping density as the basic variable. The Hohenberg-Kohn theorem rigorously proves that density can be used as the basic variable in calculating properties of the system, but does not give a recipe for how to do this. In Kohn-Sham (KS) theory this can be done by constructing an auxiliary system of hypothetical non-interacting particles that yields the same density as the true interacting system. This implies there exists some single-particle potential which when applied to noninteracting electrons, yields the same ground state density $\rho_0(r)$ as the fully interacting problem. For systems of interest in condensed matter, such a Kohn-Sham system always exists.
This fictitious system is a set of particles whose properties are identical to those of electrons, except that the electron-electron repulsive interaction is switched off. Since the interacting and non-interacting systems have the same densities and energies, $T_s[\rho]$ (the noninteracting kinetic energy) and $V_{ee}[\rho]$ can be added to and subtracted from the variational energy formula, giving expressions for the electronic energy and in particular for the exchange-correlation contribution E_{xc} to it:

$$E_{el}[\rho] = T_s[\rho] + V_{ne}[\rho] + J_s[\rho] + \Delta T[\rho] + \Delta V_{ee}[\rho] \tag{2.15}$$

$$E_{xc}[\rho] = \Delta T[\rho] + \Delta Vee[\rho] \tag{2.16}$$

The kinetic energy

$$T[\rho] - T_s[\rho] \tag{2.17}$$

this difference is the kinetic contribution to correlation.

The difference ΔV_{ee} is made up of Hartree-Fock exchange and the electrostatic contribution due to correlation. Since the E_{xc} contains all the important quantum many-body effects, the true exchange correlation functional is likely to be very complex, but in practice relatively simple approximations to it work surprisingly well in calculations.

The wavefunction for the non-interacting system can be written as

$$\Psi(\rho) = \frac{1}{\sqrt{N!}}|\psi_1(r_1)...\psi_N(r_N)| \tag{2.18}$$

When the orbitals ψ are expressed in terms of basis functions χ, a set of equations is obtained that is analogous to that employed for HF theory. The orbitals ψ that minimize $E[\rho]$ satisfy the Kohn-Sham equations:

$$\mathbf{h}_{KS}\psi_i = \varepsilon_i\psi_i \tag{2.19}$$

$$\hat{h} = -\frac{1}{2}\nabla^2 + \nu_{eff} \tag{2.20}$$

$$\nu_{eff} = \nu(r) + \int \frac{\rho(r)}{|r - r'|}dr' + \nu_{xc} \tag{2.21}$$

$$\nu_{xc}(r) = \frac{\partial E_{xc}(\rho)}{\partial\rho(r)} \tag{2.22}$$

Given an initial guess density ρ , elements of $\hat{h}_{KS}$ can be evaluated. Solution of the resulting pseudo-eigenvalue equation yields eigenvalues ε_i ("orbital energies") and eigenfunctions ψ_i (orbitals, expressed in basis functions). These lead to a new density, and iteration should converge to a self-consistent set of orbitals ψ_i and density ρ.

SCF cycle

The method described above represents the State of Art of *ab-initio* calculations as it can refine itself as we want. In order to give an idea of how an *SCF* cycle, the Kohn-Sham procedure, iterate. We put the ordered instructions to do one interaction cycle, as follows:

1. Guess an initial density;
2. Calculate the Hamiltonian from Euler-Lagrange equations in the chosen basis, and diagonalize it to get the wavefunctions and orbital energies;
3. Fill states with N Fermion particles to determine which states are occupied;
4. Construct a new density from the wavefunctions for occupied states;
5. Mix the input and output densities, for numerical stability reasons;
6. If the density has not yet converged, go to step 2.

Exchange-correlation Functional

As mentioned above, in principle E_{xc} not only accounts for the difference between the classical and quantum mechanical electron–electron repulsion, but also includes the difference in kinetic energy between the fictitious non-interacting system and the real system. In practice, most modern functionals do not attempt to compute this portion explicitly. Instead, they either ignore the term, or construct a set of *hole functions* that incorporate the kinetic energy difference implicitly. Many functionals contain empirical parameters; if they are based on experimental data they necessarily introduce some kinetic energy correction. In discussing the nature of functionals, it is convenient to adopt some of the notation commonly used in the field. The functional dependence of E_{xc} on the electron density is expressed as an interaction between the electron density and an 'energy density' ε_{xc} that depends on the electron density.

$$E_{xc}[\rho(r)] = \int \rho(r)\varepsilon_{xc}[\rho(r)]dr \tag{2.23}$$

LDA The local density approximation, (LDA), [44] was designed to be exact in the limit of a uniform electron gas. The exchange contribution for a uniform electron gas with density $\rho(r)$ is given by the Dirac exchange equation:

$$E_x = \frac{3}{4\pi}\int (3\pi^2\rho(r))^{\frac{1}{3}}\rho(r)dr \tag{2.24}$$

where

$$\varepsilon_x[\rho(r)] = \frac{3}{4}(\frac{3}{\pi})^{\frac{1}{3}}\rho(r)^{\frac{1}{3}}$$

The correlation contribution is generally fitted as an enhancement of exchange, in the form

$$E_{xc}[\rho(r)] = \int \rho(r)\varepsilon_x[\rho(r)]F_{xc}[\rho(r)]dr \tag{2.25}$$

taken from Monte Carlo simulations of a free electron gas. Most of the modern correlation functionals in use are based on Monte Carlo data published by Ceperley and Alder for the above electron gas. [13]

The next level of improvement of the exchange-correlation functional over LDA is to allow a dependence on the density gradients : E_{xc} is then calculated via

$$E_{xc}[\rho(r)] = \int \varepsilon_x[\rho(r)]F_{xc}[\rho\uparrow(r), \rho\downarrow(r), \nabla\rho\uparrow(r), \nabla\rho\downarrow(r)]\rho(r)dr \tag{2.26}$$

GGA In GGA (General Gradient Approximation) that functionals usually lead to improvements in bond lengths and lattice constants. Commonly used GGA functionals are Perdew-Wang (PW91) [40] and Perdew-Burke-Enzerhof (PBE). [30] Some correlation functionals are expressed through a gradient expansion of LSDA (Local Spin Density Approximation); this includes the LYP functional based on earlier work on exact HF correlation formula. [34]

An example of an 'empirical' functional based on GGA is the Becke exchange functional (B88): [4]

$$E_x = E_x^{LDA}[\rho(r)] - \int F_X[s]\rho^{\frac{4}{3}}dr \tag{2.27}$$

where the functional is

$$F_x = \beta 2^{-\frac{1}{3}}\frac{s^2}{1 + 6\beta\sinh^{-1}} \tag{2.28}$$

where

$$s = \frac{|\nabla\rho|}{\rho^{\frac{3}{4}}}$$

was optimized to the value of 0.0042 using Hartree–Fock exchange energies of noble-gas atoms.

Typical errors in the exchange energies are ~ 10‰for E_x^{LDA} and ~ 0.1 ‰for E_{Becke} , illustrating that gradient approximations lead to strongly improved results.

2.4.3 The Adiabatic Connection Method

If one imagines to controlling the extent of electron–electron interactions in a many-electron system from the non-interacting KS reference system to the real, interacting system, one can show that the exchange-correlation energy can be computed as

$$E_{xc} = \int \langle \psi(\lambda) | \, V_{xc}(\lambda) | \psi(\lambda) \rangle d\lambda \tag{2.29}$$

where λ describes the extent of inter-electronic interaction, ranging from 0 (none) to 1 (exact).

While we do not know V_{xc} as a function of λ, we can evaluate the left end-point of the curve ($\lambda = 0$). Here, the only component of V_{xc} is exchange deriving from asymmetry of the wave function. The Slater determinant of K-S orbitals is the exact wave function of the non-interacting Hamiltonian operator, and the exact exchange for the non-interacting system can be computed just as in HF calculations except using the KS orbitals. On going from the non-interacting to the interacting system, the total exchange-correlation energy decreases by

$$\langle \psi(1) | \, V_{cc} | \psi(1) \rangle - E_{xc}^{0} \tag{2.30}$$

Unfortunately, we do not know the expectation value of the fully interacting exchange-correlation potential applied to the fully interacting wave function. However, one could write E_{xc} for a real system as an interpolation between the value calculated by some choice of DFT functional and the "exact" HF exchange calculated from the KS wavefunction:

$$E_{xc} = E_{x}^{HF} + z(E_{xc}^{DFT} - E_{xc}^{HF}) \tag{2.31}$$

This forms the basis of the so-called *adiabatic connection method* (ACM), because it connects the non-interacting and fully interacting states. Using GGA exchange-correlation, Becke showed that the 3-parameter functional expression of the B3LYP model, [5] defined by

$$E_{xc}^{B3LYP} = (1-a)E_{x}^{LSDA} + aE_{x}^{HF} + bE_{x}^{B} + (1-c)E_{c}^{LSDA} + cE_{c}^{LYP} \tag{2.32}$$

where a, b, and c are empirically optimized values, has overall performance that is remarkably good.

Besides the B3 methods a number of one-parameter models, restricting themselves to adjusting the percentage of HF exchange included in the functional, have been proposed. These include B1PW91, [1] B1LYP [1] and PBE1 [36]; the latter is sometimes called PBE0 because the parameter dictating the percentage contribution of HF exchange, 0.25, was not empirically optimized, but instead chosen based on perturbation theory arguments, so that there are 'zero' fitted parameters. Overall, the performance of these functionals, as well as other ACM functionals listed, tends to be fairly comparable to the B3 methods. Functionals incorporating a contribution of HF exchange are called *hybrid* functionals, whereas functionals not using this are often called *pure* functionals. DFT shows systematic weaknesses in calculated geometries and energies. Thus, van der Waals complexes tend to have interfragment distances that are too large because the dispersion-induced attraction is not properly modeled (although it

may accidentally be mimicked by BSSE). [48] Hydrogen bonds are too short as a rule, and most charge transfer complexes have their polarities overestimated so that they are too tightly bound.

The Periodic Calculations

In the *quantum* simulation of solids, two approaches exist. The first one is the cluster approach. It consists in cutting out a portion of matter from the solid surface, representative enough of its key features. The main advantage is that the obtained clusters can be treated as molecules and a broad variety of ab-initio methods can be adopted, while limiting the request of computational power. The main disadvantage is that physical terminations are introduced and long-range electrostatic effects are not taken into account. The second approach, that has been adopted in this thesis, consists in treating a complex solid material as a pure crystalline material. Translational symmetry is applied to the unit cell to replicate the included atoms in 3D space within the periodic boundary conditions. The ab-initio treatment of systems with translational symmetry exploits Bloch's theorem:

$$\Psi_n^k(r+R) = \psi_n^k \exp^{i(\mathbf{k}*\mathbf{R})} \tag{2.33}$$

The quantum mechanical methods aimed to calculate energies and wavefunctions of polyatomic systems (once geometry is specified) may be also applied in calculations on crystals. In those type of calculations we look for a wavefunction that is a linear combination of basis functions. The choice of basis set determines large differences in the approach we adopt. The spreadly used basis set adopt as functions the plane waves (PW) and the atomic orbitals of isolated atoms (LCAO).
The problem of any quantum method applying to crystal solid state matter is the resolution of the Schrodinger (or Hartree) equation in a limitless system as a mere arrangement of repeating building block, called crystallographic cell, once defined the space group of the crystal it is possible to perform DFT calculations by restriction to elementary cell and hence reproducing the solution by symmetry to all lattice. The Bloch theorem [7] states that we can find, in systems characterized by a periodic potential, the wave functions is simply a travelling wave plane of real wavenumbers k as

$$\psi(k) = A \exp^{i(\mathbf{k}*\mathbf{r})} \tag{2.34}$$

It is important to note this wave behavior, as the frequency of the wave goes along k number as the k reflect the inverse of primitive unitary vector of the crystal cell. That plane waves also constitute a complete set of orthogonal function of eigenvalue

$$E(k) = \frac{h^2k^2}{(8\pi^2)m_e} \tag{2.35}$$

and so can be conveniently used as an expansion set. If we apply the Hamiltonian operator of a crystal system of

$$\frac{p^2}{2m} + \sum_{n=-\infty}^{\infty} \mathbf{v_n} \exp^{i\frac{n2\pi}{a}} \tag{2.36}$$

periodicity to a generic plane wave as described, we see that solution belongs to the subspace S_k of plane waves of wave numbers $k + h_n$.

This subspace is closed under the application of the Hamiltonian to any of its elements; thus the diagonalization of the energies matrix, ε_{ij} , it always possible and shows that S_k solution differ from $S_{k'}$ one only if $\mathbf{k}$ and $\mathbf{k}'$ are not related by integer multiples of $\frac{2\pi}{a}$. This allow us to define a fundamental region of k-space, limited by $-\frac{pi}{a} < k \leq \frac{pi}{a}$, which include all different k, named first Brillouin zone. The first Brillouin zone of the reciprocal space has the same definition as the Wigner-Seitz cell in the direct lattice: is the figure that contains all and only nonequivalents k points closer to the chosen lattice (say k=0) than any other. The shape of the Brillouin zone is connected to the geometry of the direct Bravais lattice, irrespective of the content of other information. Bloch demonstrated that any (physically acceptable) solution of the Schrodinger equation in a periodic potential takes the form of a travelling plane wave modulated on the microscopic scale by an appropriate functions (e.g. the hydrogenoid mono-electron atomic orbitals) with the lattice periodicity. Through this theorem we can easily construct orthogonal orbitals $|kn\rangle$ by considering linear combinations of atomic orbitals of the type:

$$|kn\rangle = N^{-\frac{1}{2}} \sum_{t_n} \exp^{i\mathbf{k}*\mathbf{t_n}} |\phi_{r-t_n}\rangle \tag{2.37}$$

Note that t_n is a translation vector. The function defined above is called a Bloch sum, and satisfies the Bloch theorem. The hole set of linear combinations of the k function described, also known as tight-binding wavefunction, constitute a complete set of Hamiltonian solutions in that k point, span a subspace of the Hilbert space and have the great advantage that they do not mix under the influence of a periodic potential. Commonly only a part of k points are used, these numbers are chosen due to allow fast calculus and realistic results. The secular equation expressed in these functions can be written as:

$$\sum [\mathbf{H^k_{jj}} - \varepsilon_k \mathbf{S^k_{jj}}] c_{j'kn} = 0 \tag{2.38}$$

The computational code that was employed for all the ab-initio calculations in the present thesis was the CRYSTAL09 code. It is based on a LCAO treatment of periodic systems: the Bloch functions are expanded as linear combinations of atom-centered Gaussian functions. With this code one keeps periodicity by periodic boundary conditions as stated by the Bloch theorem have the resolution of the wavefunction of interest. The resolution itself of any mono-electronic function by means of the Kohn-Sham equation is therefore done in the associated reciprocal space. More specifically, each Crystalline Orbital, $\phi_i(r,k)$, is a linear combination of Bloch functions (BF), $\Phi(r,k)$, defined in terms of local functions (Atomic Orbitals, AO), $\phi_\mu(r)$:

$$\Psi_i(r,k) = \sum_\mu a_{\mu,i}(k)\phi_{mu}(r,k)$$

$$\phi_{mu}(r,k) = \sum_g \phi_{mu}(r - A_{mu} - g) \exp^{i(\mathbf{k}*\mathbf{g})} \tag{2.39}$$

The local functions are expressed as linear combinations of a certain number, n_G , of individually normalized Gaussian type functions characterized by the same centre, with fixed coefficients, d_j and exponents, α_j , defined in the input.

$$\phi_{mu}(r - A_{mu} - g) = \sum_{j}^{n_G} d_j G(\alpha_j, r - A_{mu} - g) \tag{2.40}$$

By using Bloch functions it is possible to split the crystal problem in separate problems for each k hence the expansion coefficients of the Bloch functions, $a_{mu,i}(k)$, are calculated by solving the matrix equation for each reciprocal lattice vector, k:

$$\mathbf{F}(\mathbf{k})\mathbf{A}(\mathbf{k}) = \mathbf{S}(\mathbf{k})\mathbf{A}(\mathbf{k})\mathbf{E}(\mathbf{k}) \tag{2.41}$$

Since this thesis deals with surfaces, the adopted model is the so-called slab model. Periodic boundaries conditions are applied only in two dimensions: the thickness of the resulting surface (or slab) is finite, while periodicity is bi-dimensional generating an infinite plane.

Geometry Optimization Techniques

The performance of the various functionals is usually quite good when comes to predicting minimum-energy structures. A simple-minded approach for minimizing a function is to proceed step to step in varying one variable until the function reach a minimum, and then switch to the next one. However, several cycles are necessary to find a structure that represents a stationary point on a multidimensional energy surface so that this method is unacceptably inefficient. Essentially all commonly used methods assume that at least the first derivative of the energy with respect to all variables, the gradient g, can be calculated analytically. Some methods also assume that the second derivative of the energy, the Hessian, **H**, is available. The steepest descent method lowers the energy by stepping opposite to where the gradient vector g points. This works but is also rather inefficient. Most modern algorithms are based on the Newton-Raphson approach and require knowledge of the first derivative as well as an approximation to the second derivative. In spite of this, analytic first derivatives are available for almost all density functionals and can be calculated efficiently. In contrast, calculation of second derivatives (analytical or numerical) is rather expensive, and is not done frequently, if at all, during minimization. Instead, an updating scheme is used. The idea is to start with an approximated Hessian, and as the optimization proceeds, the gradients at the previous and currents point are used to improve the approximation. There are many updating schemes; some of the commonly used ones are Davidon-Fletcher- Powell (DFP), Broyden-Fletcher-Goldfarb-Shanno (BFGS) [9, 10, 17, 21, 43] and Powell. [29] For minimization BFGS is often preferred as it tends to keep the Hessian positive definite.

A thermodynamical point of view

The energy calculated above describe only in part the thermodynamical energy, because of the Born-Oppenheimer approximation in which systems are studied, all energies arising from the motion of nuclei including their zero-point vibrational energies are omitted in what we called total electron energy. By the use of some concepts of thermodynamics and statistical mechanic there is the possibility to get all the needed nuclear energies. Statistical mechanics allows calculation of the translational, rotational and vibrational energy and entropy contributions. As described in the next section, the determination of the whole

Hessian matrix, representing the force constant in the harmonic oscillatory let us to calculate the eigenvectors associated and the energy of each vibrational mode. When a vibrational analysis is done also the determination of entropy become possible through the use of the proper partition function.

$$S_{vib} = R \sum_{i=1}^{3N-6(7)} \left(\frac{h\nu_i}{kT} \frac{1}{\exp^{\frac{h\nu_i}{kT}} - 1} - ln(1 - \exp^{\frac{h\nu_i}{kT}}) \right) \tag{2.42}$$

Finally we can, by simple thermodynamics arguments, evaluate the real total energies of each structure.

Vibrational normal modes

Every atomic nucleus is always moving, also in the solid state. Calculate how one can decompose the vibration moving in the vibrational modes, gives us a reach set of information about their vibration levels energies, about their stabilities. In order to calculate the vibration wave function that dictate the nuclei behavior we have to do some crude approximations such as this eigenvectors extend to all the crystal building. The potential energy, that feel nuclei, can be approximated by a second-order Taylor expansion around the stationary geometry

$$v_{eff} = v_{eff}(r_0) + v_{eff}(r - r_0) + \frac{1}{2}(r - r_0)^t v_{eff}(r - r_0) + ... \tag{2.43}$$

The energy for the expansion point, $\mathbf{V_{r_0}}$, may be chosen as zero and the first derivative is zero since r_0 is a stationary point.

$$\mathbf{V_{r_0}} = \frac{1}{2}(r - r_0)\mathbf{V}''(r - r_0) = \frac{1}{2}(r - r_0)\mathbf{F}(r - r_0) \tag{2.44}$$

Here $\mathbf{F}$ is the $N_{atom}x3$ second-derivative matrix (Hessian). The nuclear Schrodinger equation for an N atoms system is given by:

$$\left[-\sum (\frac{1}{2m_i} \frac{\partial^2}{\partial r_i^2}) + \frac{1}{2}(r - r_0)\mathbf{F}(r - r_0) \right] \Psi_{nuclear} = E_{nuclear}\Psi_{nuclear} \tag{2.45}$$

This equation is first transformed to mass-weighted coordinates by a $\mathbf{G}$ matrix containing the inverse square root of atomic masses, in line with the Born-Oppenheimer assumption that electrons instantly follow the nuclei.

$$\left[-\sum (\frac{1}{2m_i} \frac{\partial^2}{\partial y_i^2}) + \frac{1}{2} y(\mathbf{F} * \mathbf{G})y \right] \Psi_{nuclear} = E_{nuclear}\Psi_{nuclear} \tag{2.46}$$

A unitary transformation is used to diagonalize the F*G matrix, yielding eigenvalues ε_i and eigenvectors q_i. The kinetic energy operator is still diagonal in these coordinates.

$$\left[-\sum (\frac{1}{2m_i} \frac{\partial^2}{\partial q_i^2}) + \frac{1}{2} q^t(\mathbf{U}(\mathbf{F} * \mathbf{G})\mathbf{U^t})q \right] \Psi_{nuclear} = E_{nuclear}\Psi_{nuclear} \tag{2.47}$$

where

$$q = \mathbf{U}y$$

In the q-coordinate system, the $3 \cdot N$ atom dimensional Schrodinger equation separates into 3N atom one-dimensional Schrodinger equations, which are just in the form of a standard harmonic oscillator. The eigenvectors q_i of the $F * G$ matrix are the mass- weighted vibrational normal modes and their eigenvalues ε_i are related to the vibrational frequencies by

$$v_i = \frac{1}{2\pi}\sqrt{\varepsilon_i} \tag{2.48}$$

There should be six eigenvalues of exactly zero (five for linear molecules), corresponding to the translational and rotational modes. If the stationary point is a minimum on the energy surface, the remaining eigenvalues are all positive. If, however, the stationary point is a transition state (TS), one (and only one) of the eigenvalues is negative; this corresponds to the energy being a maximum in one direction and a minimum in all other directions. The frequency for the vibration, obtained from the equation 2.48, along this eigenvalue will be imaginary as it is the square root of a negative number. The corresponding eigenvector is the direction leading downhill from the TS towards reactant and product.

Basis Sets

In practice, application of DFT requires that the wave function is expressed as a Slater determinant formed from the individual occupied, the Kohn-Sham orbitals. These orbitals are then expanded in some set of basis functions. There are a large variety of basis sets; some of the most widely used are plane waves (PW), [3, 24, 31, 47, 49, 55] local orbitals (LO), [8, 16] linearized augmented plane waves (LAPW) [14] and linearized muffin-tin orbitals (LMTO). [33] The *Kohn-Sham limit* is achieved by use of an infinite basis set, which would yield the best orbitals and electron probability density for the chosen functional. In practice, one cannot use of an infinite basis set. Much work has gone into identifying mathematical functions that allow wave functions to approach the KS limit closely in as efficient a manner as possible. Efficiency in this case involves three considerations. The number of two-electron integrals that need to be calculated increases as N^4 where N is the number of base functions. So, keeping the total number of base functions small is computationally attractive. In addition, however, it is useful to choose basis set functions that permit the various integrals appearing in the KS equations to be evaluated efficiently. Thus, a larger basis set can still represent a computational improvement over a smaller basis set if evaluation of the greater number of integrals for the former can be carried out faster than for the latter. Finally, the base functions must be chosen to have a form that is useful in a chemical sense. That is, the functions should have large amplitude in regions of space where the electron probability density (the wavefunction) is also large, and small amplitudes where the probability density is small. The simultaneous optimization of these three considerations is at the heart of basis set development. Slater-type orbitals (STOs) were introduced as the basis functions used in extended Hückel theory. They have a number of attractive features primarily associated with the degree of resemblance to hydrogen atomic orbitals. However, there is no analytical expression for general four-index integrals involving STOs. Their cumbersome numerical evaluation severely limits utility of STOs in molecular systems of any significant

size. Boys proposed Gaussian-type orbitals (GTOs) [8] as an alternative to the use of STOs. Four-index integrals involving GTOs are much easier to evaluate than those involving STOs. The general functional form of a normalized Gaussian-type orbital (GTO) in atom-centered Cartesian coordinates is

$$\varphi(x,y,z,\alpha,i,j,k) = (\frac{2\alpha}{\pi})(\frac{3}{4})[\frac{(8\alpha)i+j+ki!j!k!}{(2i)!(2j)!(2k)!}]^{\frac{1}{2}} \\ x^i y^j z^k \exp^{-\alpha(x^2+y^2+z^2)} \quad (2.49)$$

where α is an exponent controlling the width of the GTO, and i, j, and k are non-negative integers that dictate the nature of the orbital in a Cartesian sense.

Although they are convenient from a computational standpoint, GTOs have specific features that diminish their utility as basis functions. One issue of key concern is the shape of the radial portion of the orbital. For s type functions, GTOs are smooth and differentiable at the nucleus ($r = 0$), but real hydrogen AOs have a cusp. In addition, all hydrogen AOs have a radial decay that is exponential in r while the decay of GTOs is exponential in r^2; this results in too rapid reduction in amplitude with distance for the GTOs. In order to combine the best feature of GTOs (computational efficiency) with that of STOs (proper radial shape), most basis sets used nowadays use "contracted" basis functions, each consisting of several GTOs combined to have an improved (often STO-like) behaviour as a function of r:

$$\chi(x,y,z,\alpha,i,j,k) = \sum_a c_a \varphi_a(x,y,z,\alpha,i,j,k) \quad (2.50)$$

The coefficients c are chosen to optimize the shape of the basis function sum and ensure normalization. It is important to note that although the base functions on each individual atom are orthogonal to each other, basis functions on crystal atoms are not orthogonal. For a crystal, the overlap matrix has the form

$$\mathbf{S}^k_{ij} = \delta_{ij} + \sum \langle R_i | 0_j \rangle \exp^{i(mathbf k*(R+s_i-s_j))} \quad (2.51)$$

where s_i locates the i-th atom in the unit cell, and R is a Bravais lattice vector, so that the vector $R + s_i - s_j$ goes between the i-th atom in the unit cell at the origin and the j-th atom in the unit cell located at R.

The overlap matrix is not the identity matrix because the tail of a basis function on one atom overlaps the tail of base functions on other atoms.

Chapter 3

Polycaprolactone thermodynamics

Although many studies declare itself to be capable of handling hydrogen bonds in polymer solutions, often this theories appear descriptive. As matter of fact they deal with macroscopic nature of systems and materials. A unification between microscopic and macroscopic model is still a matter of controversy. Starting with thermodynamics theories allow us to calculate macroscopic properties of system in exam as accurately as possible but much less accuracy can be found in the microscopic observables. Our need is to explore the phase space of a system, bringing us to as a reasonable model as force field methods. Then we start to describe the configurational space by the trajectories provided by molecular dynamics. This let to provide *macroscopic* properties as function of *microscopic* ones. Microscopic properties are properly refined in a quantum fashion.

3.1 Introduction

In this work we mainly focused on Poly$-\varepsilon-$caprolactone, a polyesters prepared by ring opening polymerization of lactones, its commercial behavior in Figure 3.1.

Polyesters are coming into prominence as a results of their environmental sustainability. Such macro-molecules are intrinsically different from the other. Their structures can be influenced in that the chains has a sense of direction by the uniform orientation of the ester groups in the chains, as we can see in the next chapter at section 4.3.2. Depending on the distance between the ester groups in the chains and their interactions, one can find different intra- or inter-molecular interactions and then different arrangement of the chains.

Figure 3.1: Polycaprolactone polymer in commercial pellets form

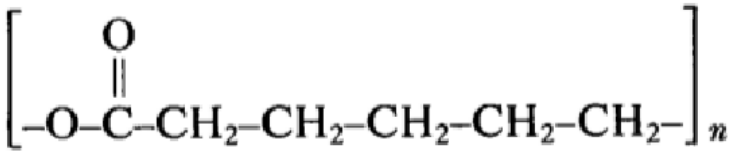

Figure 3.2: Repeating unit of polycaprolactone polymer

Poly$-\varepsilon-$caprolactone, made by ring opening polymerization of ε-caprolactone, has the structure reported in figure 3.2, and it therefore possesses one of the larger repeating units so far studied in polyesters.

Poly$-\varepsilon-$caprolactone, is a biocompatible and biocompatible thermoplastic polymer [15, 50, 53] that melts at 60 ℃. Semycrystalline at room temperature, then with low T_g (in the range from about -60 ℃to -40 ℃) [15], this polymer is relatively hydrophobic and, among biodegradable polymers, exhibits low water solubility [22, 46] which results in a relatively good barrier to moisture. It has receiving attention over the years in the view of its technological relevance in several fields such as the productions of bio-medical scaffolds as for the development of a new generation of biomaterials for tissue engineering like *3D printing*. Its use as biomedical scaffold is approved by Food and Drug Administration. For any biocompatible polymer the issue of water diffusion is of paramount importance, since it controls the degradation's behavior and the ease with which this may be integrated within a living organism. A detailed understanding of the water transport mechanism requires specific informations at the molecular level, such as the number and structure of the molecular aggregates. Modelling of equilibrium adsorption thermodynamics for such systems should hence explicitly account for specific hydrogen bonding (HB).

3.2 The thermodynamics approach

We perform an analysis of thermodynamics of water adsorption in rubbery polymers in the present section using a *lattice fluid* theory including the effect of possible self- and cross- interactions in polymer-penetrant systems. In particular, we use, as wrote in theory chapter, here the "nonrandom lattice fluid hydrogen bonding" (NRHB) theory developed by Panayiotou [11, 12, 27] based on the factorization of the partition function in two separate contributions: one related to *mean field* interactions and one accounting for the effects of specific (HB) interactions.

$$Z = Z_R Z_{NR} Z_{HB} \tag{3.1}$$

The first two contributions are constructed starting from the idea that the partition function, related to *mean field* interactions, can be further factorized out into an ideal random contribution and in a nonrandom contribution that is obtained treating each kind of contact as a reversible chemical reaction (*quasi chemical* approximation)[23]: nonrandomness of all the possible couple of contacts between *mers* of the components of the mixture as well as hole sites is assumed.

The second contribution, accounting for the effect of Hydrogen-Bond interactions, is formulated by using a combinatorial approach first proposed by Veytsmann.[51]

We focus here on the phase equilibrium between a binary rubbery polymer-water mixture and pure water in a vapor phase, since the polymer is assumed to be not soluble within the gaseous phase. Establishment of this equilibrium implies the equality of the chemical potentials of water in the two coexisting phases.

The expressions of chemical potential in both phases are coupled with the proper expressions for the equation of state (EOS) of both phases. Here and in the following we will consider only binary mixtures, with subscript 'A' referring to water and subscript 'B' referring to polymer. Relevant parameters of the model[2] are k_{AB}, that is, the mean-field lattice fluid interactional parameter which measures the departure from the geometric mean of the mixing rules for the characteristic energies of the lattice fluid:

$$\varepsilon^*_{AB} = (1 - k_{AB})\sqrt{\varepsilon^*_{AA} + \varepsilon^*_{BB}}. \tag{3.2}$$

According to the NRHB model, the water chemical potential in the polymer-water mixture and in the pure water phase is expressed as the sum of a *mean field* contribution and a HB contribution:

$$\mu_A = \mu_{A,MF} + \mu_{A,HB} \tag{3.3}$$

Where, as mentioned in the theory chapter, the chemical potential for physical and specific contact is given by:

$$\frac{\mu_{i,MF}}{RT} = \ln\frac{\phi_i}{\omega_i r_i} - r_i\sum_j^t \frac{\phi_j l_j}{r_j} + \ln\tilde{\rho} + r_i(\tilde{\nu}-1)\ln\left[1-\tilde{\rho}\right] + \\ - r_i\frac{z}{2}\left[\tilde{\nu}-1+\frac{q_i}{r_i}\right]\ln\left[1-\tilde{\rho}+\frac{q}{r}\tilde{\rho}\right] + \\ + \frac{zq_i}{2}\left[\ln\Gamma_{ii} + \frac{r_i}{q_i}(\tilde{\nu}-1)\ln\Gamma_{00}\right] - \frac{q_i}{\tilde{T}} + r_i\cdot\frac{\tilde{P}\tilde{\nu}}{\tilde{T}} + \\ + r_i\nu_H - \sum_{\alpha=1}^{m} d_\alpha^i + ln\frac{\nu_d^\alpha}{\nu_{\alpha 0}} - \sum_{\beta=1}^{n} a_\beta^i + ln\frac{\nu_a^\beta}{\nu_{\beta 0}} \quad (3.4)$$

For the meaning of all the symbols we remaind to the section 1.1.8.

The corresponding equations of the chemical potential for the pure componets can be calculated by setting, at a given reduced temperature and pressure, the closed packed volume fraction of the component i, ϕ_i and allowing the summation over only one component.

When the mixture system reach the equilibrium with the liquid/vapour water phase, their chemical potential are equal. Therefore one can calculate at a given reduced pressure and reduced temperature the density of the mixture system at equilibrium by using the equation 3.4 and giving retry values for the non random state variables, Γ_{00} and Γ_{11}. It is worth noting that ω_i and l_i are characteristic quantities for the i component.

Then we can calculate the number of hydrogen bonds in the system by applying the reduced density find before in the equation of state for the mixture.

$$\tilde{P} + \tilde{T}\left[\ln(1-\tilde{\rho}) - \tilde{\rho}\cdot\left(\sum_i^t \phi_i\frac{l_i}{r_i} - \nu_H\right)\right] + \\ - \tilde{T}\frac{z}{2}ln\left[1-\tilde{\rho}+\frac{q}{r}\tilde{\rho}\right] + +\tilde{T}\frac{z}{2}ln\Gamma_{00} = 0 \quad (3.5)$$

with ν_H being the hydrogen bonding contact number following the formula:

$$\nu_H = \sum_\alpha^m\sum_\beta^n \nu_{\alpha\beta} = \sum_\alpha^m\sum_\beta^n \frac{N_{\alpha\beta}}{rN}. \quad (3.6)$$

Further, we minimize the number of hydrogen bond contact minimizing, for all hydrogen acceptor and donor group, the reported condition:

$$\frac{\nu_{\alpha\beta}}{\nu_{\alpha 0}\nu_{0\beta}} = \tilde{\rho}\exp^{-\frac{G^H_{\alpha\beta}}{RT}} \quad (3.7)$$

where

$$G^H_{\alpha\beta} = E^H_{\alpha\beta} + PV^H_{\alpha\beta} - TS_{\alpha\beta}.$$

$E_{\alpha\beta}$, $S_{\alpha\beta}$ and $V_{\beta\alpha}$ representing, respectively, the molar internal energy of formation, the molar entropy of formation, and the molar volume change upon formation of hydrogen bonding between the proton donor group of type α and the proton acceptor group of type β. E_{AA} and S_{AA} have been taken as being the same both in the vapor and in the polymer mixture phase and are available

from the literature.[2] In the present context, V_{AB} and V_{AA} have been taken to be equal to zero according to the assumption made by in recent publications.[2] On the basis of polymer chemical structure (absence of hydrogen-bond donor groups on the polymer backbone) we infer that self-HB only occurs between water molecules, both in the pure water vapor and in the polymer-water mixture. Hence N_{AA}^{v} and N_{AA}^{wp}, are the only number of self-HB to be considered, where subscripts v and wp indicate the vapour phase and the mixture respectively. Moreover, based on the outcomes of the spectroscopic analysis, it can be deduced that only two type of hydrogen-bond acceptor group is present on the polymer backbone and one type of HB donor group is present on a water molecule. As a consequence, considering that the polymer is not present in the vapor phase, N_{AB}^{wp} is the only variable related to cross-HB, that occurs between water and polymer molecules in the polymer-water mixture. In the following, the variables that we will consider when comparing model with experiments are actually a slight reformulation of the N_{ij}. In fact, referring to the polymer-water phase, it will be considered in the analysis the number of moles of water self-HB per mass of amorphous phase of PCL and the number of moles of cross HB occurring between the proton donor groups of water molecules and the proton acceptor groups present on the PCL backbone, normalized as well per mass of amorphous phase of PCL.

The state variables Γ_{00} and Γ_{AA}, are the nonrandom factor for the distribution of contacts in the given mixture and can be calculated by using their minimization equations. In particular, the state variables Γ_{00} and $\Gamma 11$ appear in the equations, that are, respectively, the nonrandom factors for the distribution of an empty site around another empty site and of molecular segments of penetrant around a molecular segment of the penetrant itself, in the two phases at equilibrium.

In summary, the set of equations to be solved to determine the water solubility in PCL according to the NRHB model is the following:

- Equivalence of chemical potentials of penetrant in the gas phase (μ_{GAS_A}) and polymer phase (μ_{POL_A}).
- EOS for the vapor and for the polymer mixture phases.
- Equations for the number of hydrogen bonds established in the two phases at equilibrium with N_{ij} representing the total number of hydrogen bonding interactions between proton donor groups of type i and proton acceptor groups of type j.
- Equations for the nonrandom factors for the distribution of contacts in the lattice.

This model has been used to fit experimental adsorption isotherms of water in PCL, assuming as fitting parameters k_{AB}^{wp} E_{AB}^{wp} , and S_{AB}. The solution of this system of equations supplies, at fixed values of pressure and temperature, the density of the two phases, the values of Γ_{00} and Γ_{AA} variables in the two phases, the concentration of penetrant in the polymer-penetrant mixture, the number of each type of hydrogen bonds in the vapor phase and in the water-polymer mixture, that is, N_{AA}^{v},N_{AA}^{wp} and N_{AB}^{wp}. It is important to note that, as for any theory based on EOS, one needs to know the scaling parameters for pure water and pure polymer. In fact, for the case of PCL, lattice fluid scaling parameters

for pure polymer (i.e, $\varepsilon^*_{h_B}$, $\varepsilon^*_{s_B}$ and $\nu^*_{sp,B}$) have been determined by the fitting of PVT data for PCL using the NRHB EOS equation, while lattice fluid scaling parameters for water (i.e, $\varepsilon^*_{h_A}$, $\varepsilon^*_{s_A}$ and $\nu^*_{sp,A}$) E_{AA} and S_{BB} have been taken from the literature [52] and are assumed to be the same in the water vapor and in the water/polymer mixtures (i.e., $E^w_{AA} = E^{wp}_{AA}$ and $S^{0w}_{AA} = S^{0w}_{AA}$). It is important to note that the NRHB model is based on the Lattice Fluid framework which is suitable for totally amorphous rubbery polymers and does not account for the presence of crystalline domains. For the sake of interpretation of experimental water adsorption isotherms in semicrystalline PCL crystals are modeled as being impervious to water molecules and to compare data with model predictions the overall solubility measured in the semicrystalline samples has been re-scaled to obtain that of the pure amorphous PCL, accounting for the presence of the impervious crystalline fraction. It has been, hence, assumed that the presence of crystals does not alter the thermodynamic behavior of the amorphous domains.

3.2.1 Analysis

The NRHB model has been used to interpret water adsorption thermodynamics in PCL. As already mentioned, the concentration of water has been normalized to the fraction of amorphous phase of the polymer, assuming that the solubility in the crystalline phase is negligible and that the presence of crystals do not alter the thermodynamic behavior of the amorphous domains. In applying the NRHB approach, we have imposed that the volume change upon formation of water self-HB and water/polymer cross-HB are zero (both in the water/polymer mixture and in the vapor phase in contact with it), according to the assumption made by the authors of NRHB in recent publications.[11]

Application of NRHB to the PCL/water system and its use for fitting of gravimetric adsorption isotherms are thoroughly discussed in Figure 3.3 cation by Scherillo et al [2] and we briefly recall the results to focus then on the comparison of model predictions with the results of spectroscopic analysis. Fitting parameters for NRHB model to be determined from experimental adsorption isotherms of water in PCL are $k_{AB}, E^{wp}_{AB}, and S_{AB}$. Lattice fluid scaling parameters for pure PCL (i.e, $\varepsilon^*_{h_B}$, $\varepsilon^*_{s_B}$ and $\nu^*_{sp,B}$) have been determined by the fitting of PVT data for PCL using the NRHB model for pure fluids and their values are reported in the following table.

substance	$\varepsilon^*_h[\mathbf{J/mol}]$	$\varepsilon^*_s[\mathbf{J/(mol * K)}]$	$\nu^*_{sp,0}[\mathbf{cm^3/g}]$
PCL	5876 ± 50	3.824 ± 0.001	0.8873 ± 0.005

Lattice fluid scaling parameters for water (i.e, $\varepsilon^*_{h_A}$, $\varepsilon^*_{s_A}$ and $\nu^*_{sp,A}$),$E^w_{AA} = E^{wp}_{AA}$ and $S^w_{AA} = S^{wp}_{AA}$ have been taken from the literature [52] and are in the following table.

substance	$\varepsilon^*_h[\mathbf{J/mol}]$	$\varepsilon^*_s[\mathbf{J/(mol * K)}]$	$\nu^*_{sp,0}[\mathbf{cm^3/g}]$
H_2O	5336.5	-6.506	0.9703

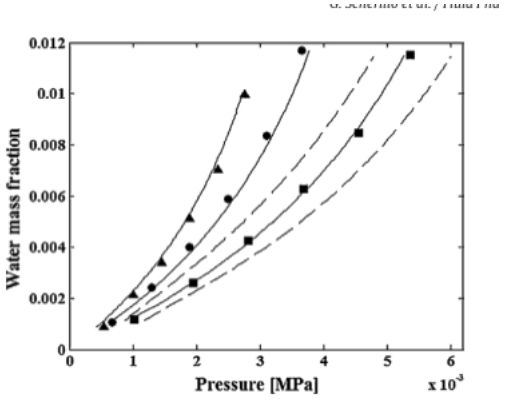

Figure 3.3: Fitting curves providing isotherms for PCL by NRHB model

On the basis of the spectroscopic analysis, it has been assumed that a one proton acceptor group (i.e., carbonyl group) is present per repeating unit of the polymer and that two equivalent proton donor groups and two equivalent proton acceptor groups are present on each molecule of water. PCL along with experimental data at 25, 30, and 37 ℃, the NRHB model provides a good fitting of experimental data. Best fitting parameters are reported in Table.

k_{AB}	$E_{AB}[\mathbf{J}/(\mathbf{mol})]$	$S_{AB}[\mathbf{J}/(\mathbf{mol} * \mathbf{K})]$
-0.1152 ± 0.005	-11130 ± 200	-6.13 ± 0.1

Once the model parameters were determined from the fitting of the gravimetric data, the NRHB model was used to predict quantitatively the amount present in the polymer/water mixture, in equilibrium with a water vapor phase, of self-HB formed by water molecules and of cross-HB established between carbonyls and water molecules at 25 and 30℃. As can be inferred, the moles of HB established at 30 ℃within the polymer/water mixture, normalized by the mass of amorphous polymer, are reported, in Figure 3.4, as a function of the water mass fraction; also in this case the model provides a reasonable estimate of the number of hydrogen bonds formed, etching a good agreement with values for cross-HB evaluated in the hypothesis of the ½stoichiometry of the carbonyl-water adduct. However, the a caution should be applied in drawing conclusions about actual involvement of a single water molecule in bridging two PA groups present on macro-molecules.

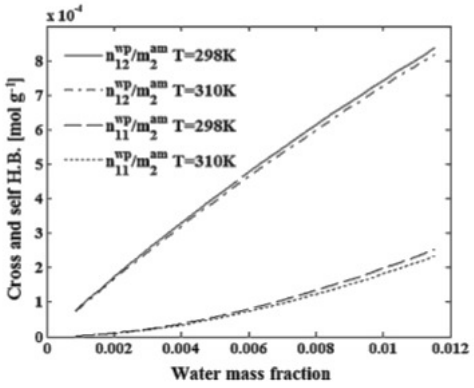

Figure 3.4: Number of HB contacts between mer and water provided by NRHB model

Chapter 4

Pure components

In describing the thermodynamics properties of liquid systems often we use descriptive and approximate theories, remarkable strikes have been made with the liquid theories derived from the Flory and Huggins works, which culminates with the Panayiuotou theory of fluids and others the end up in formulating an equation of state of the a component in a system. Such theories are called EOS theory. NRHB provide a detailed descriptions of pure fluids and their mixtures previous a fitting machinery to determine the parameters involved in their description. More deeply, any pure fluid needs at least six parameters in order to have a NRHB equation of state. Three of them concern the non-specific interactions described in the theoretical chapter like as first argued by Sanchez-Lacombe and three other concerning the theoretical parameters introduced by Panayioutou mainly due, according to the theory, the hydrogen bonds present. With the aim of testing the above equation of state in complex systems, we proceed to analyze in more detail the hydrogen bond thermodynamics present in as a pure liquid as pure methanol, water and poly-ε-caprolactone. Then we extend this treatment to poly-ε-caprolactone water mixture.

4.0.2 Computational Methods

As we want to have a molecular dynamics model able to reproduce phase stucture of pure components and expecially of mixtures, the best choice in term of computational time saving and in term of accurancy is to use the molecular dynamics to explore that phase space. Therefore we are interested to build an atomistic model of bulk phases. Molecular dynamics program, through user customization give an output of several configurations time-dependant, called trajectory, we assume represent a typical phase space evolution at the given temperature and pressure.

Molecular dynamics

In describing the thermodynamics properties of liquid systems often we use descriptive and approximate theories, remarkable strikes have been made with the liquid theories derived from the Flory and Huggins works, which culminates with the Panayiuotou theory of fluids (hereinafter NRHB) and others the end up in formulating an equation of state of the a component in a system. Such

theories are called EOS theory. The NRHB need six parameters for each pure compound. Three of them concern the non-specific interactions described in the theoretical chapter like as first argued by Sanchez-Lacombe and three other concerning the theoretical parameters introduced by Panayioutou mainly due, according to the theory, the hydrogen bonds present. With the aim of testing the above equation of state in complex systems, we proceed to analyze in more detail the hydrogen bond thermodynamics present in as a pure liquid as pure methanol and water.

Ab-initio calculations

A detailed study is made to investigate the specific and non specific interaction between molecules in the liquid. to be written

4.1 Methanol

As we want to have a molecular dynamics model able to reproduce phases structures of polymer-penetrant mixtures of poly-caprolactone, the best choice is to start with a simple model of a bulk phase as pure liquid as methanol. Methanol is a light-weighted alcohol, often present as result of fermentation and as industrial reagent. Its hazardous nature to human health, made this reagent a deeply feared and studied reagent.

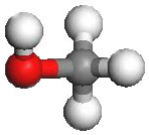

Figure 4.1: Methanol molecule in a ball and stick representation

4.1.1 NRHB fitting

As already detailed in the theoretical background chapter, scaling paramenters for methanol have been obtained by fitting experimental PVT data with NRHB equation of state. Data minimization has been performed using a Levenberg-Marquardt minimization algorithm which operates by comparing experimental densities with those predicted theoretically, which have been calculated by using a Newton-Raphson method to solve equations for equilibrium density. In figure 4.13 are reported the experimental data and fitted NRHB diagrams of P(T) and T(D) functions.

NRHB EoS parameters for methanol component have been obtained by fitting PVT data using NRHB for pure fluids, mean filed parameters.

$\varepsilon_h^*[Jmol^{-1}]$	$\varepsilon_s^*[Jmol^{-1}K^{-1}]$	$v_{sp,0}^*[cm^3g^{-1}]$
4187.5	2.2E-14	1.121

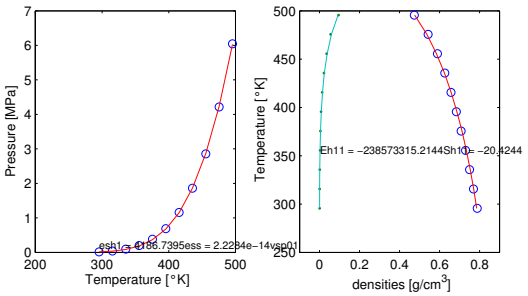

Figure 4.2: Fitting of the experimental pressure volume temperature data

NRHB EoS parameters for methanol component have been obtained by fitting PVT data using NRHB for pure fluids, specific interaction parameters.

$E^0_{11}[Jmol^{-1}]$	$S^0_{11}[Jmol^{-1}K^{-1}]$	**s**
-23860	-20.42	0.941

Molecular dynamics

The model is builded and integrated by means of velocity verlet algorithm in DlPOLY software package.

DLPOLY4 is a general purpose serial and parallel molecular dynamics simulation package originally developed at Daresbury Laboratory by W. Smith and T.R. Forester under the auspices of the Engineering and Physical Sciences Research Council (EPSRC) for the EPSRC's Collaborative Computational Project for the Computer Simulation of Condensed Phases (CCP5) and the Molecular Simulation Group (MSG) at Daresbury Laboratory. The package is the property of the Central Laboratory of the Research Councils. This program throught user customization give an output of several configurations time-dependant, called trajectory, we assume represent a typical phase space evolution at the given temperature and pressure.

System definition The system, we want to simulate, is made up of 153 methanol molecule, (CH_5O). The simulation box is constructed using *Amorphous Cell* software function of *Material Studio* program suite. The suite draws a cubic box of randomly rotated molecules. These latter are as build as to explore the more relevant conformers allowed by their degrees of freedom at the given temperature and pressure (SATP condition). The periodic cell, choiced as cubic shaped, have a *cell* parameter of 2.297 nm.

The given structure coordinates are used to build a potential field that we are aimed to use with the molecular dynamics simulation. Their reciprocal connections are used to build *force field* of the model that fully describe the force acting on each of the 918 atoms provided in the box. To build these relations we use *DLFIELD* program, which, although through the user-defined topology of the single molecule, easily build a relations ensemble ready to molecular mechanics or simulations. The *force field*, describing the relative relations from the atoms

are based on UDFF parameters [54], they describe the system as points moving in harmonic potentials for the intra-molecular forces and in central potential fields for the inter-molecular forces.

```
MOLECULE methanol 6 99.0 ! Methanol
C1  CH3_aliphatic    H1
H1  H_nonpolar       |
H2  H_nonpolar   H3−C1−O1−H4
O1  O_alcohol        |
H4  H_alcohol        H2
H3  H_nonpolar
CONNECT C1 > H1 H2 H3 O1
CONNECT H1 > C1
CONNECT H2 > C1
CONNECT O1 > C1 H4
CONNECT H4 > O1
CONNECT H3 > C1
END MOLECULE
```

Initial velocities are imposed to the particles by a Maxwellian distribution at the proper temperature. The box needs several minimizations to avoid particles overlapping. To this aim, the steepest descendant method is adopted. The velocity verlet algorithm has set to a time step of 1fs. A Hoover thermostat is used at temperature of 273℃and a isotrpic proper barostat is set to 1 atm.

Equilibration The random generate structures of the model need to be *equilibrated*, that is to be in equilibrium with the forces acting on the system. At the first step energy seems as to be disappeared in the model as it goes to equilibrate the potential fields describing the system. Then the model sees its temperature decrease. To reach equilibrium, an algorithm create energy in the system or destroy at every step. This algorithm is called themostat and barostat, it decrease or increase velocity of atoms in the system until the temperature and pressure are stable and therefore in equilibrium. The mathematical model behind the computational machinery need to be equilibrated to avoid numerical instabilities too. To check if the model reach the equilibration we analyze the volume behaviour and realize equilibrated system, as we can see in figure 4.3 as density start to be fluctuating around a constant value.

The density of the system is one of the most east property to calculate. It is easy in fact to obtain the box dimension. Therefore, the volumes and the densities are easily calculate each step over the trajectory. Even so, it is one of the most important properties to state the validity of a microscopic model, since it is related to whole interactions between particles. The experimental data are found in litterature[52].

The constant value of density of methanol liquid at 273℃is $0.96664 \pm 4.37E-5 g * cm^{-3}$. The experimental value of density reported [52] is $0.7863 g * cm^{-3}$.

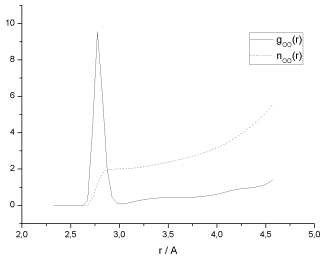

Figure 4.4: Radial distribution function (g) of oxygen atoms around the oxygen atom in a methanol molecule

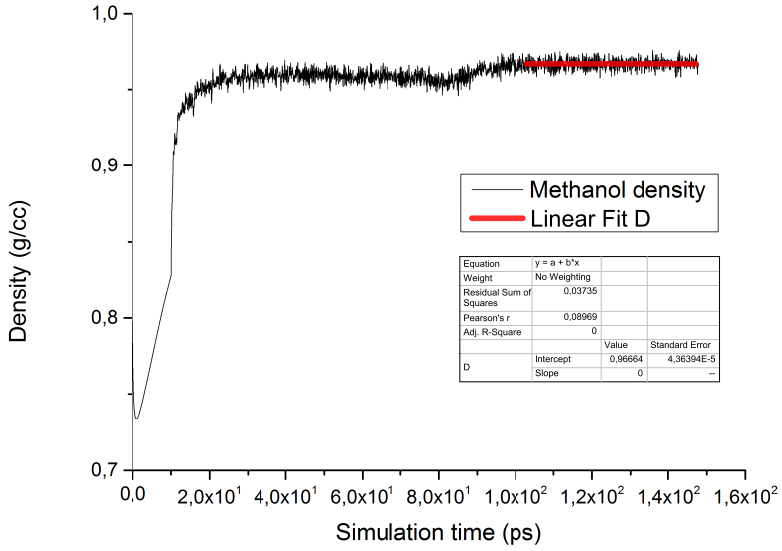

Figure 4.3: Density evolution diagram as function of time simulation and it predicted value

Analysis of the trajectory provide us a tool to determine the typical interacting distances between methanol molecules in a specific type interaction such as hydrogen bond. Radial distribution functions deal with the distributions of molecules in the simulation box and therefore describe the phase space of an interaction of interest. Radial distribution function of the hydrogen atom in the hydroxyl group around oxygen atom, reported in figure 4.5 tell us the interacting distance is of 1.8 $\mathring{A}$. Further consideration lead to integrate this curve to obtain that almost the hydrogen capable groups present in the liquid are interacting.

Through a Fortran90 code, written for the purpose, able to read the program

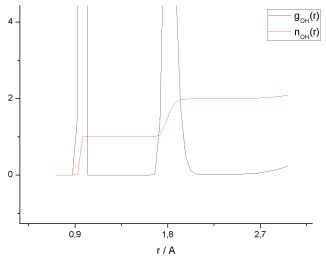

Figure 4.5: Radial distribution function (g) of hydroxylic hydrogen atoms around the oxygen atom in a methanol molecule

history, we analyze the phase space to determine the interactional dimers of interest. This program is reported in Appendix A. Therefore with the proper distance between donor and acceptor hydrogen bond group and extract the wanted structures.

4.1.2 A quantum refinement

Structures produced, analyzed and extracted by molecular dynamics as described in the previous section are imported in a much more descriptive methods such as quantum *ab-initio*. In order to give the best resemblance to experimental data we choice the well tested Density Fuctional theory method to describe the extracted dimers. These structures are to imported in *ab-initio* program, GAMESS-UK. This later open-source have been exploited as to have a much better control over any phase of calculation. *GAMESS is a program for ab-initio molecular quantum chemistry. Briefly, GAMESS can compute SCF wavefunctions ranging from RHF, ROHF, UHF, GVB, and MCSCF. Correlation corrections to these SCF wavefunctions include Configuration Interaction, second order perturbation Theory, and Coupled-Cluster approaches, as well as the Density Functional Theory approximation. Excited states can be computed by CI, EOM, or TD-DFT procedures. Nuclear gradients are available, for automatic geometry optimization, transition state searches, or reaction path following. Computation of the energy hessian permits prediction of vibrational frequencies, with IR or Raman intensities. Solvent effects may be modeled by the discrete Effective Fragment potentials, or continuum models such as the Polarizable Continuum Model. Numerous relativistic computations are available, including infinite order two component scalar relativity corrections, with various spin-orbit coupling options. The Fragment Molecular Orbital method permits use of many of these sophisticated treatments to be used on very large systems, by dividing the computation into small fragments. Nuclear wavefunctions can also be computed, in VSCF, or with explicit treatment of nuclear orbitals by the NEO code.*

4.1.3 H-bond dimer

With the structures previous analyzed and extracted from molecular dynamics through a home-written code, able to read the trajectory, then determine

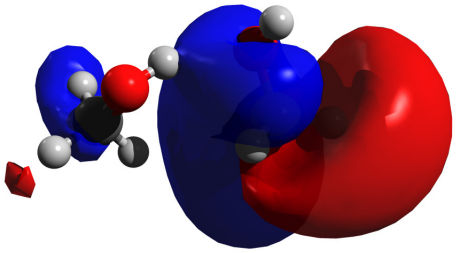

Figure 4.6: Shape of HOMO orbital in a HB methanol dimer, showed to stabilize electron density on the hydrogen atom

the interactional distance between donor and acceptor hydrogen bond group and choice the wanted structures to be extracted. The specific interactional structures are used as geometry input to a *Density Functional Theory* calculations to determine the total electron stabilization energy. Method we used is an hybrid functional, B3LYP plus an additive term, due to Grimme, intended to deal with short-range forces acting as on the electrons in the system as London forces. These kind of forces are of relevant importance in describing the molecular fluids where most of the phase cohesion forces have their origin from the forces of van der Waals. Further we abbreviate these method as *B3LYP-D2*. Basis sets choiced are all as *triple zeta* plus dispersion as 6-311g++ *Pople* basis. *H-bond* dimers were analyzed with GAMESS-UK program.

Non-optimized structures Commonly, quantum *ab-initio* calculations start from fully optimized geometries that describe as the *hypothetical* stationary shape of molecules as derived from Born-Oppenheimer approximation. This latter approximation dictates the nuclear motions too slow to interact with the electrons behaviour. As matter of fact, all *ab-initio* calculations provide well described wave function near to 0°Ctemperature, thus the structures provide by optimization method commonly used, are the minimum energy structures no dealing with nucleus's motion. Then the structures provided by molecular dynamics are a bit from stationary so classical energy evaluations cannot be applied and therefore, previous the wave function calculation. Thus an optimization of nuclears coordinates calculation is done.

Reasonable energy value is given by way deals with the reported formulation:

$$\Delta E_{h-bond} = E_{dimer} - 2 * E_{monomer}$$

Where the term in the right side of equation related to optimized structures. We report the calculated energies for the hydrogen bond of methanol dimer.

Struct.	$\Delta E_{B3LYP-D2}$	ΔE_{B3LYP}	ΔE_{vdw}
H1	-41.404	-31.223	-9.963
H2	-41.200	-30.908	-10.292
H3	-40.821	-29.293	-11.528
mean	-41.069	-30.475	-10.594

Reported energy variations are in $KJ * mol^{-1}$ unit.

Vibrational analysis Reported results give a reasonable value of energies variations involved in a hydrogen bond formation in gas phase. But as more parameters are needed by Panayiotou theory as three energy variation related to this specific bond formation, more deeply they are: an inner energy variation; a volume variation and then an entropy variation. In order to calculate the entropy variation we have to evaluate the energy of all accessible quantum level and then calculate as the entropy as result of their proximity to room temperature energy. Electron excited level are not feasible at SATP then their contribution to entropy in not relevant. Further rotational and translation energy level, their entropy related energy too, can be easily calculated by simple statistical mechanics formula. More in trouble is to deal with vibrational quantum level, vibrational analysis is the much feasible method to evaluate the all vibrational level energy as described in previous chapter. Simply we have to determine the *Hessian* matrix by numerical derivation of the first analytic functional derivative, that matrix, in the harmonically approximation, represent the motion constrain of all atoms. Further we can deal with the probability occupation of higher vibrational level than ground state at a wanted temperature. Need to outlined need to run this calculations on previous optimized structures. Reported entropy energy variations and zero-point inner energy variations are reported.

Struct.	ΔE_0	ΔE_{therm}	ΔS_{tra}	ΔS_{rot}	ΔS_{vib}
H1	7.678	10.458	-143.335	-52.202	83.039
H2	7.322	7.935	-143.335	-52.256	62.288
H3	6.869	7.704	-143.335	-52.391	65.371
mean	7.290	8.699	-143.335	-52.283	70.233

Reported energy variations are in $KJ * mol^{-1}$ unit and for entropy variations, (ΔS), are in $J * mol^{-1} * K^{-1}$.

Vibrational analysis permit to evaluate total electron energy variations.

Struct.	$\Delta E_{B3LYP-D2}$	ΔE_{B3LYP}	ΔE_{vdw}
H1	-31.223	-20.765	-9.963
H1	-33.265	-22.973	-10.292
H1	-33.117	-21.589	-11.528
mean	-32.370	-21.776	-10.594

Reported energy variations are in $KJ * mol^{-1}$ unit.

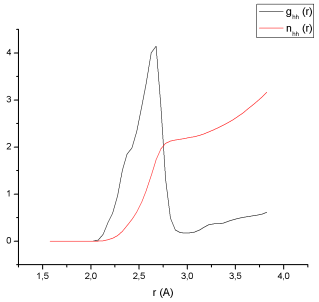

Figure 4.7: Radial function of hydrogen atoms around hydrogen atoms

4.1.4 Van der Waals dimer

Hydrogen bond formation interested happens in solutions, therefore short-range forces that appear to be more important than long-range electrostatic forces, rule very less in energy formation of hydrogen bond when molecule are in a condensed phase like liquid than in a gas phase. Indeed molecule in solution interacts continuously by van der Walls forces, that is, the main force that aggregates non polar molecule in liquid phase. Clearly we need a strategy to calculate the energy variations in a *mean field* liquid involved in formation of an hydrogen bond. The basic idea is to separate the contributions of the mean field from that of the specific interactions.

Van der Walls dimer extractions Short-range dimers are to be the starting point to deal with any thermodynamic theory of fluid. Through the radial distribution function, g(r), reported in figure 4.7, we depict a strategy analysis to find and extract van der Walls dimer.

The much populated distance in the figure is $4.4\mathring{A}$ between the carbon atoms of two molecules. We then assumed this distance, as the most explored in specific interaction structures and therefore the more relevant in the thermodynamic properties. With the same trajectory previous analyzed in order to extract the specific interaction dimers from molecular dynamics, through the home-written code, able to read the trajectory, we determine the interactional distance between carbon and carbon atoms and choice as the wanted structures to be extracted as the structures that interact for a distance of $4.4\mathring{A}$, we choice as 25 structure as a good way to approximate the averaged thermodynamic value. The structures are grafically tested to eliminates any occurrence of hydrogen bonded structures.

Optimized dimer Dimeric structures provided by molecular dynamics are a bit from stationary so classical energy evaluations cannot be applied. Then their structure are provided as starting geometry to a DFT/B3LYP-D2 calculations with a 6-311(G)++ basis sets function. The basis sets used are the same Pople basis sets used in the specific calculations.

$$\Delta E_{vdW} = E_{dimer} - 2 * E_{monomer} \tag{4.1}$$

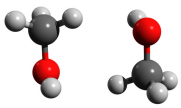

Figure 4.8: Dimer structure of two methanol related by an inversion symmetry point

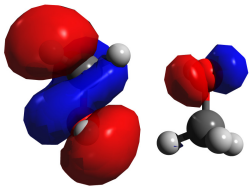

Figure 4.9: Shape of HOMO orbital in an inversion related methanol dimer

Many dimer optimization ended in hydrogen bonded structure, and in another specific interaction structure where the two molecule are related by an inversion symmetry point, that is one molecule is the reflection through a point of the other. This way allow to get a zero value summation of their dipole moments. Structure is reported in figure 4.8.

Such dimers are to be excluded in non specific interaction, as they occur only in a particular orientation and the stabilization of electric field generated by dipole moments sees it depletition by solvent effect. Thus in solution methanol dimer dipole moments are stabilized by long range electric forces generated by methanol dipole itself. The Homo orbital donates electron density on the *methane like* orbital of the CH_3 group, this can be viewed in the reported figure /refinv-orb.

Struct.	$\Delta E_{B3LYP-D2}$	ΔE_{B3LYP}
D1	-15.44	-3.67
D3	-14.52	-3.78
D7	-5.23	-3.67
D8	-13.04	-6.38
D16	-14.26	-1.74
D17	-14.46	-3.56
D19	-14.43	-2.98
D21	-13.15	-4.62
D25	-14.03	-2.40
mean	-13.17	-2.83

Reported energy are in $K * J * mol^{-1}$.

A vibrational analysis is also conducted on the optimized structures of methanol dimers. This allow estimate of thermodynamical properties of the non-specific interaction. Note that entropy variations, in the tranlsation, are all equal for the reactions since theirs involved the same reaction, then these latter have a value of:

$$\Delta S_{tra} = 143.34 J * (mol * K)^{-1}.$$

Struct.	ΔE_0	ΔS_{rot}	ΔS_{vib}
D1	4.764	-50.63	67.78
D3	5.136	-50.54	88.88
D7	2.230	-51.35	71.33
D8	3.922	-49.01	83.28
D16	4.683	-50.38	77.39
D17	5.480	-50.49	89.31
D19	5.103	-50.54	89.70
D21	3.633	-49.40	59.24
D25	4.192	-50.57	50.65
mean	4.35	-50.32	75.28

Reported energy variations are in $KJ * mol^{-1}$ unit and for entropy variations, (ΔS), are in $J * mol^{-1} * K^{-1}$.

Vibrational analysis permit to evaluate total electron energy variations.

Struct.	ΔE_{B3LYP}	$\Delta E_{B3LYP-D2}$	ΔE_{vdw}
D1	-11.60	-9.12	2.48
D3	-8.11	-5.64	2.48
D7	-4.57	-2.09	2.48
D8	-9.24	-6.76	2.48
D16	-10.18	-7.70	2.48
D17	-7.88	-5.41	2.48
D19	-8.04	-5.56	2.48
D21	-11.96	-9.48	2.48
D25	-12.77	-10.30	2.48
mean	-9.38	-6.89	2.48

Reported energy variations are in $KJ * mol^{-1}$ unit.

Hydrogen bond in mean field

Energy contribution due the formation of a specific interaction between an hydrogen atom, poor of electron density, and an electron rich atom such as oxygen is know as hydrogen bond. In gas phase its formation is mainly driven by electrostatic force acting as to orientate the two molecule as to reduce the coulomb field. Then the involved energies variatios are simple calculated by subtraction of the energy of the two isolated and optimized fragments from the optimized dimer, that is the reported formula above. In liquid phase, it cannot be the same due the interactions present before the hydrogen bond formation between the two molecule. Our research simply have its starting point in the idea to

calculate the mean field interaction energy, ε and subtract it from the HB interaction term. That is, to relate the energy variation involved in hydrogen bond formation to the prior constituent such as *van der Walls* dimers.

$\Delta E_{B3LYP-D2}$	ΔE_{B3LYP}	ΔE_0	ΔE_{therm}	ΔS_{tra}	ΔS_{rot}	ΔS_{vib}
-25.48	-25.23	-0.25	2.94	0	-1.96	-5.05

Reported energy variations are in $KJ * mol^{-1}$ unit and for entropy variations, (ΔS), are in $J * mol^{-1} * K^{-1}$.

Another way to calculate the entropy variation, suggested by Panayiotou and co, is to consider it as the rotational entropy loss in the dimerization. Although the three degrees of rotational freedom are lost in dimerization, their degrees of freedom become three degrees of vibration freedom. Therefore, cause these created energy levels have a much more energy demand to be accessed, the possibility of the occupation, of highter levels than the ground state level, decrease and thus the total entropy of the system decrease. In matter of fact that their less accessibility than rotational degrees. Entropy energy variations can be calculated by subtracting the entropy contribution of the three fluffy modes created to the rotational entropy of a monomer as in the relation:

$$\Delta S_{lf,HB} = \sum_{i=1}^{3} S_{rot,i} - \sum_{i}^{3} S_{vib,i} \tag{4.2}$$

where

$$S_{rot} = R\left(\frac{3}{2} + ln\left(\frac{\sqrt{\pi}}{\sigma}\left(\frac{8\pi^2 kT}{h^2}\right)^{\frac{3}{2}}\sqrt{I_1 I_2 I_3}\right)\right) \tag{4.3}$$

$$S_{vib} = R\left(\frac{h\nu_i}{kT}\frac{1}{\exp^{\frac{h\nu_i}{kT}}-1} - ln(1-\exp^{\frac{h\nu_i}{kT}})\right) \tag{4.4}$$

4.1.5 Interpetration of calculated data

As already detailed in the theoretical background chapter, scaling paramenters for methanol have been obtained by fitting experimental PVT data with NRHB equation of state. Data minimization has been performed using a Levenberg-Marquardt minimization algorithm which operates by comparing experimental densities with those predicted theoretically, which have been calculated by using a Newton-Raphson method to solve equations for equilibrium density. In figure 4.11 are reported the experimental data and fitted NRHB diagrams of P(T) and T(D) functions.

The calculated internal energy variations and entropy variations for methanol, reported in table,

NRHB EoS parameters for methanol component for pure fluids, specific interaction parameters.

$E_{11}^0[Jmol^{-1}]$	$S_{11}^0[Jmol^{-1}K^{-1}]$
-21780	-20.92

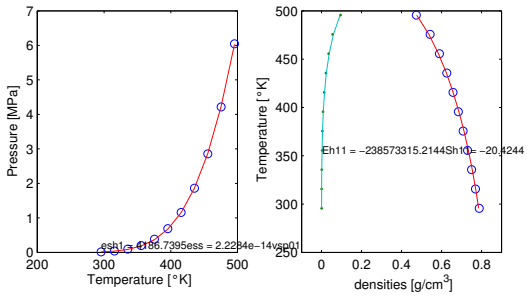

Figure 4.10: Fitting of the experimental pressure volume temperature data of methanol fluid

are then used to fit experimental data as reported in figure 4.11.

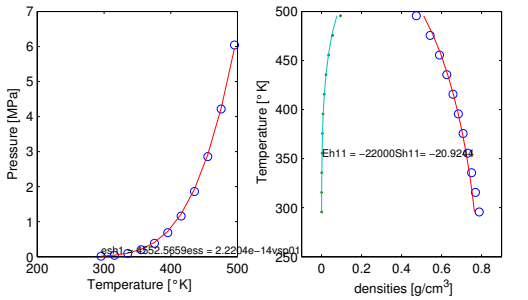

Figure 4.11: Fitting of the experimental pressure volume temperature data of methanol fluid with specific interaction parameters calculated

NRHB EoS parameters for methanol component using NRHB for pure fluids, mean filed parameters.

$\varepsilon_h^*[Jmol^{-1}]$	$\varepsilon_s^*[Jmol^{-1}K^{-1}]$	$v_{sp,0}^*[cm^3g^{-1}]$	**s**
4553	2.2E-14	1.180	0.941

4.2 Water

Water is as widely spreaded as of human importance molecule. As we want to have a molecular dynamics model able to reproduce phases structures of polymer-penetrant mixtures of poly-caprolactone, then the most stable poly-caprolactone-solvent is with water molecules, where they stabilize the liquid sol making a network well established of hydrogen bonds.

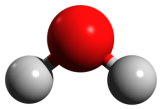

Figure 4.12: Water molecule

4.2.1 NRHB fitting

As already detailed in the theoretical background chapter, scaling paramenters for water have been obtained by fitting experimental PVT data with NRHB equation of state. Data minimization has been performed using a Levenberg-Marquardt minimization algorithm which operates by comparing experimental densities with those predicted theoretically, which have been calculated by using a Newton-Raphson method to solve equations for equilibrium density. In figure 4.13 are reported the experimental data and fitted NRHB diagrams of P(T) and T(D) functions.

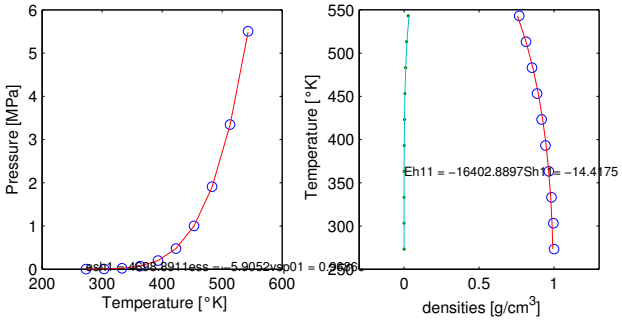

Figure 4.13: Fitting of the experimental pressure volume temperature data

NRHB EoS parameters for water component have been obtained by fitting PVT data using NRHB for pure fluids. The mean field parameters are:

$\varepsilon_h^*[Jmol^{-1}]$	$\varepsilon_s^*[Jmol^{-1}K^{-1}]$	$v_{sp,0}^*[cm^3g^{-1}]$	**s**
4699	-5.905	0.9886	0.861

NRHB EoS parameters for water component have been obtained by fitting PVT data using NRHB for pure fluids. The specific interaction parameters are:

$E_{11}^0[Jmol^{-1}]$	$S_{11}^0[Jmol^{-1}K^{-1}]$
-16400	-14.42

In order to get the structure we have to study the macroscopic environment of pure water liquid through molecular mechanics model.

4.2.2 Molecular dynamics

A realistic model is made up by the use of Material Studio subroutine Amorphous Cell that allow us to create a a model is made up of 500 water molecule, (H_2O). The simulation box is constructed using *Amorphous Cell* software function of *Material Studio* program suite. The suite draws a cubic box of randomly rotated molecules. These latter are as build as to explore the more relevant conformers allowed by their degrees of freedom at the given temperature and pressure (SATP condition). The periodic cell, choiced as cubic shaped, have a *cell* parameter of 2.422 nm. The given structure coordinates are used to build a potential field that we are aimed to use with the molecular dynamics simulation. Their reciprocal connections are used to build topology of the model molecule and then are used to create the *force field*, that is the list of all the acting forces on each of the 1500 atoms provided in the box. describing the model. To build these relations we use *DLFIELD* program, which, although through the user defined topology of the single molecule, easily build a relations ensemble ready to molecular mechanics or simulations.

```
Force Field of water generated by DL_FIELD v3.10
Units kcal/mol
Molecular types 1
Molecule name not_define
nummols 700
atoms 3
o*          15.99940    -0.79820   1   0
hw           1.00797     0.39910   1   0
hw           1.00797     0.39910   1   0
bonds 2
quar    1    2  1126.56000    0.97000 -4284.66000 7608.48000
quar    1    3  1126.56000    0.97000 -4284.66000 7608.48000
angles 1
quar    2    1    3    99.68000   103.70000   -34.80000   -32.00000
finish
vdw 3
o*      o*      nm      0.2740          9          6      3.6080
hw      o*      nm      0.0034          9          6      3.2148
hw      hw      nm      0.0130          9          6      1.0980
close
```

The *force field*, describing the relative relations from the atoms are based on UDFF parameters, [54] they describe the system as points move in harmonic potentials for the intra-molecular forces and in central potential fields for the inter-molecular forces. A Langevin thermostat is used at temperature of 298℃.

Equilibration The random generate structures of the model need to be *equilibrated*, that is to be equilibrium with the forces acting on the system. At the first energy seems as to be disappeared in the model as it goes to equilibrate the potential fields describing the system. As the model sees its temperature decrease, the mathematical model behind the computational machinery equilibrate the system rescaling the the particles velocities. Such calculations are made up by DL-POLY program. To check if the model reach the thermodynamic equilibrium we analyze the volume behaviour and realize equilibrated system as density start to be fluctuating around a constant value. The constant value of density of methanol liquid at 298℃is $1.01313 \pm 6.9E-4g*cm^{-3}$.

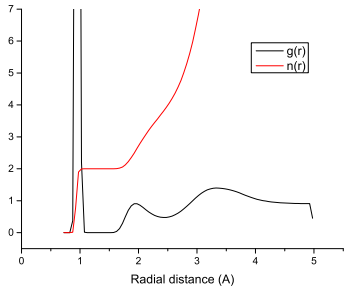

Figure 4.15: Radial distribution function of hydrogen atom around oxygen and its integrated function

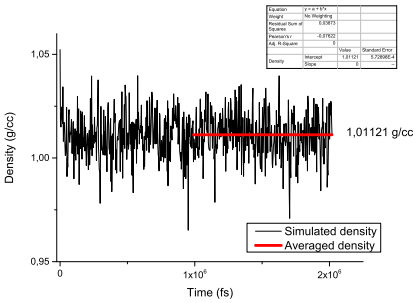

Figure 4.14: Density evolution in function of time simulation and it predicted value

Analysis of the trajectory provide us a tool to determine the typical interacting distance between water molecules in a specific type interaction such as hydrogen bond. Radial distribution function of the hydrogen atom around oxygen atom, reported in figure 4.15 tell us the interacting distance is of 3.8 $\mathring{A}$. Further considerations lead to integrate this curve to obtain that almost the hydrogen capable groups present in the liquid are interacting.

A quantum refinement The trajectory the molecular dynamics gives is like a curve that explore the phase space. As many time the system have a given set of reciprocal coordinates gives reason as a more stationary complex. Structures extracted by molecular dynamics can be analyzed through quantum *ab-initio* calculations in order to deal with their stability and their energy variations in more detail.

4.2.3 H-bond dimer

With the structures previous analyzed and extracted from molecular dynamics through a home-written code, able to read the trajectory and then determine the interactional distance between donor and acceptor hydrogen bond group, we

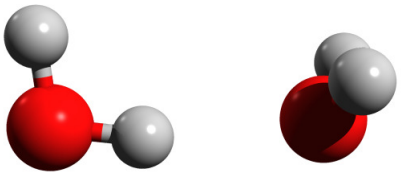

Figure 4.16: Water specific dimer optimized structure

choice the wanted structures to be extracted. The specific interactional structures are used as geometry input to a *Density Functional Theory* calculations to determine the total electron stabilization energy. Method we used is an hybrid functional, B3LYP plus an additive term intended to deal with short-range forces acting as on the electrons in the system as discussed before. Further we abbreviate these method as *B3LYP-D2*. Basis sets choiced are all as *triple zeta* plus dispersion as 6-311g++ *Pople* basis. *H-bond* dimers were analyzed with GAMESS-UK program.

ΔE_{B3LYP}	$\Delta E_{B3LYP-D2}$
-35.224	-39.659

Reported energy variations are in $KJ * mol^{-1}$ unit.

Vibrational analysis Reported results give a reasonable value of energies variations involved in a hydrogen bond formation in gas phase. But as more parameters are needed by Panayiotou theory as three energy variation related to this specific bond formation, more deeply they are: an inner energy variation; a volume variation and then an entropy variation. In order to calculate the entropy variation we have to evaluate the energy of all accessible quantum level and then calculate as the entropy as result of their proximity to room temperature energy. Electron excited level are not feasible at SATP then their contribution to entropy in not relevant. Further rotational and translation energy level, their entropy related energy too, can be easily calculated by simple statistical mechanics formula. More in trouble is to deal with vibrational quantum level, vibrational analysis is the much feasible method to evaluate the all vibrational level energy as described in previous chapter. Simply we have to determine the *Hessian* matrix by numerical derivation of the first analytic functional derivative, that matrix, in the harmonical approximation, represent the motion constrain of all atoms. Further we can deal with the probability occupation of higher vibrational level than ground state at a wanted temperature. Need, to outlined, is to run this calculations on previous optimized structures. Reported entropy energy variations and zero-point inner energy variations are reported.

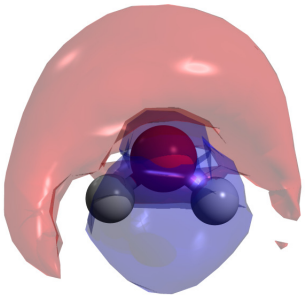

Figure 4.17: Water HOMO orbital shape capable of the strong hydrogen bond behaviour

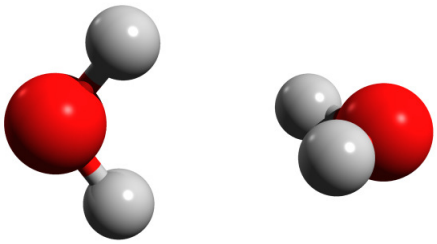

Figure 4.18: Water non specific dimer with symmetry constrain

Struct.	ΔE_0	ΔE_{therm}	ΔS_{tra}	ΔS_{rot}	ΔS_{vib}
HB	9.390	7.507	-136.155	-11.016	33.071

Reported energy variations are in $KJ * mol^{-1}$ unit and for entropy variations, (ΔS), are in $J * mol^{-1} * K^{-1}$.

4.2.4 Van der Walls dimers

Despite many dimers structures can be found in which the intermolecular interaction occurs by non specific forces. Any attempts to have an optimization of their coordinates fail. Water molecules, are composed by two hydrogen and one oxygen atoms, but it is worth noting that the main fraction of van der Walls surface are due to oxigen atom with its two lone pairs, as reported in figure 4.17.

In order to have a mean field interacting water dimers, we use symmetry operations to force the optimization to the desired result. In fact we used the rotational symmetry axis C_2 such as to prevent the approach of the atoms of hydrogen to the electrons lone pairs on the oxigen atom of the other molecule of water, the structure is represented in figure 4.18.

ΔE_{B3LYP}	$\Delta E_{B3LYP-D2}$
-3.652	-13.545

Reported energy variations are in $KJ * mol^{-1}$ unit.

Vibrational analysis Reported results give a reasonable value of energies variations involved in a hydrogen bond formation in gas phase. But as more parameters are needed by Panayiotou theory as three energy variation related to this specific bond formation, more deeply they are: an inner energy variation; a volume variation and then an entropy variation. In order to calculate the entropy variation we have to evaluate the energy of all accessible quantum level and then calculate as the entropy as result of their proximity to room temperature energy.

Struct.	ΔE_0	ΔE_{therm}	ΔS_{tra}	ΔS_{rot}	ΔS_{vib}
vdW	10.366	6.076	-136.155	-16.781	16.199

Reported energy variations are in $KJ * mol^{-1}$ unit and for entropy variations, (ΔS), are in $J * mol^{-1} * K^{-1}$.

4.2.5 H-bond in mean field

This formula used is

$$\Delta E = E_{el,hb} - E_{el,vdw} + E_0^{newNormalMode} + E_{therm}^{newNormalMode} + E_{therm,hb} - E_{therm,vdW} \tag{4.5}$$

As discussed above an vibrational analysis is only possible with a 0℃optimized structure, well describe in an harmonical approximation. Due to the small volume of hydrogen atoms in the molecule and their orbital coefficient (as we can see in Figure 4.17, van der Walls surface is an electron rich surface in this model, that result in none way to optimize an non specific interaction dimer. All the extracted and investigated dimer end their optimization in an specific interaction shape. As result to deal with entropy variations involved we use the idea developed by Panayiotou that entropy variation related in specific interactions due to the loss of rotational degrees. Dacitare Then to calculate the entropy variation we suppose, in the chosen reaction, the entropy variate as the loss of 3 rotational degrees and the formation of tree new vibrational degrees. These latter are very stiffness and can be easily found as their harmonic energies are very low. Further we use:

$$\Delta S = \sum_i^3 S_{vib,}^{i-Mode} - \sum_i^3 S_{rot,i} \tag{4.6}$$

where

$$S_{rot} = R\left(\frac{3}{2} + ln\left(\frac{\sqrt{\pi}}{\sigma}\left(\frac{8\pi^2 kT}{h^2}\right)^{\frac{3}{2}}\sqrt{I_1 I_2 I_3}\right)\right) \tag{4.7}$$

$$S_{vib} = R\sum_{i=1}^{3N-6(7)}\left(\frac{h\nu_i}{kT}\frac{1}{\exp^{\frac{h\nu_i}{kT}}-1} - ln(1-\exp^{\frac{h\nu_i}{kT}})\right) \tag{4.8}$$

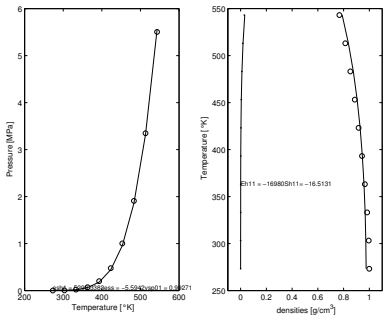

Figure 4.19: Pure water PVT data fitting with calculated parameter E

ΔE	ΔS
-16.950	-9.40

Reported energy variations are in $KJ * mol^{-1}$ unit and for entropy variations, (ΔS), are in $J * mol^{-1} * K^{-1}$.

4.3 Poly−ε−caprolactone

Poly−ε−caprolactone made by ring opening polymerization of ε-caprolactone has the following structure:

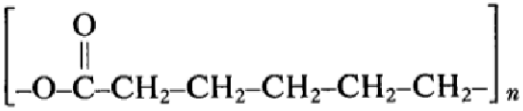

Figure 4.20: Repeating unit of polycaprolactone polymer

Polycaprolactone (PCL) is an aliphatic polyester composed of hexanoate repeat units. It is a semicrystalline polymer with a degree of crystallinity which can reach 69The unit cell is orthorhombic. The physical, thermal and mechanical properties of PCL depend on its molecular weight and its degree of crystallinity. This polymer is coming into prominence as a results of their sustainability. PCL biodegrades within several months to several years depending on the molecular weight, the degree of crystallinity of the polymer, and the conditions of degradation. Many microbes in nature are able to completely biodegrade PCL. Such macro-molecules are intrinsically different from the other conventional polyesters. Semycrystalline at room temperature, then with low T_g, it has receiving attention over the years in the view of its technological relevance in several fields such as the productions of biomedical scaffolds as for the development of a new generation of bio-materials for tissue engineering like *3D printing*. In this section a preliminary work to assemble and test the model to describe poly-ε-caprolactone. The unit cell and the chain arrangement in the crystalline state were investigated by means of periodic ab-initio calculation.

4.3.1 Molecular Dynamics

The trajectory to be analyzed are taken from the a molecular mechanics velocity verlet calculation in a NPT ensemble integrated through NAMD program.

System definition

The system, we want to simulate, is constituted by 1 poly-ε-caprolactone polymer molecule as long as 877 repeating units. The total mass of the polymer molecule is of 100 K Dalton, this value is comparable to very good commercial polymer today on hte market. We operate this choice to avoid any interactions between head and tail polymer groups with the central repeating units of the polymer. This choice is also a challenge to test big polymer molecular dynamics. The model is build in a periodic fashion with a cubic box with the polymer described above and the use of *Amorphous Cell* subroutine of Material Studio software package. The molecule is as build as to explore the more relevant

conformers allowed by their degrees of freedom at the given temperature and pressure (SATP condition). The periodic cell, choiced as cubic shaped, have a *cell* parameter of 52,557 nm. The given structure coordinates are used to build a potential field that we are aimed to use with the molecular dynamics simulation. Their reciprocal connections are used to build topology of the model molecule and then are used to create the *force field*, that is the list of all the acting forces on each of the 17789 atoms provided in the box. describing the model. To build these relations we use *PSFGEN* program, which, although through the user defined topology of the single molecule, easily build a relations ensemble ready to molecular mechanics or simulations.

The *force field* used is due to CHARMM 27 of MacKerell.[42] The topology used is reported in appendix C.

Equilibration

The molecular mechanics model have to equilibrated for long time, typically as 50 ns, in order to reach a good agreement with real data. Equilibration time can be checked with the analysis of volume or energy variations with time.

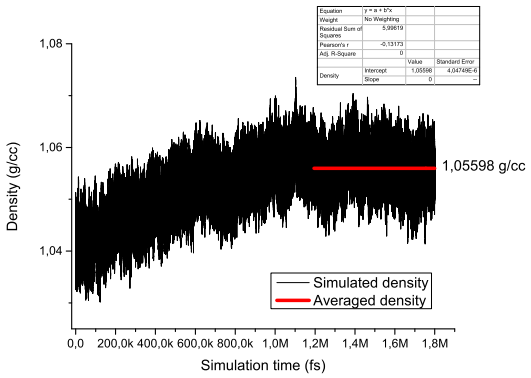

Figure 4.21: Density of amorphous Polyεcaprolactone polymer simulated

Structure	$d[g \cdot cm^{-3}]$
Amorphous PCL	1.05598

Densities calculated with molecular dynamics not agree with the experimental data present in literature and measured. The main obstacle is obviously the semi-crystalline behavior of the interest polymer. In the next section a work intended to model the crystal fashion of the polymer is presented.

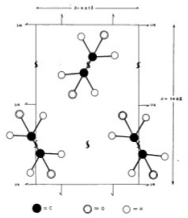

Figure 4.22: Crystal structure of Poly-ε-caprolactone polymer along the 001 plane

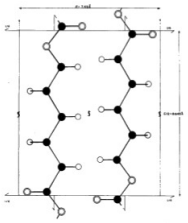

Figure 4.23: Crystal structure of Poly-ε-caprolactone polymer along the 010 plane

4.3.2 Ab-initio crystal calculations

Poly-ε-caprolactone is a semicrystalline polymer with a degree of crystallinity which can reach 69As mentioned previous, to deal with measured values one should involve an estimation of the crystal polymer density. Therefore a periodic *ab-initio* calculation is done. The method exploited is a *periodic* Density Functional Theory augmented with a semi-empirical Grimme potential. These latter have to be used aimed to describe the attractive dispersion forces acting on molecular system, especially on the apolar molecular system, where they comes to be the most important forces giving the right cohesion force to observe crystalline phase. The crystal habit of polycaprolactone is the orthorhombic crystallographic group $P2_12_12_1$, This crystallographic group is the same of the αpoly-ethylene, that is, as reported in litterature,[6] the chains are arranged parallel each other along the c axis, the fiber axis, but with opposite orientation (*up* and *down*) as we can see in figure 4.22. This unit cell is only compatible with an extended planar chain conformation of the molecule involving two monomer residues related by a twofold screw axis in the chain direction. The physical, thermal and mechanical properties of PCL depend on its molecular weight and its degree of crystallinity.

The structure calculations have been done with CRYSTAL09 software package.

Cell	a	b	c
cal	6.88	4.81	17.04
exp	7.47	4.98	17.05

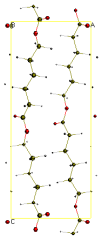

Figure 4.24: Relaxed crystal structure of Poly-ε-caprolactone polymer along the 010 plane

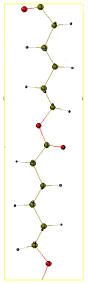

Figure 4.25: Relaxed crystal structure of Poly-ε-caprolactone polymer along the 100 plane

A crystal density, through the model previously exposed, was soon estimated in $1.342 g/cm^3$. Then a better agreement with experimental data can be achieved, therefore

$$V_{total} = V_{crystallographicphase} + V_{amorphousphase} \tag{4.9}$$

as inter-facial density between the phase can be assumed as linear as crystal composition.

$$V_{total} = (\frac{m_{cryst}}{m_{cryst}})V_{cryst} + (\frac{m_{amorph}}{m_{amorph}})V_{amorph} \tag{4.10}$$

$$\frac{V_{total}}{m_{total}} = (\frac{m_{cryst}}{m_{total}})(\frac{V_{cryst}}{m_{cryst}}) + (\frac{m_{amorph}}{m_{total}})(\frac{V_{amorph}}{m_{amorph}}) \tag{4.11}$$

Substitute the individual specific volume and massive fraction as:

$$\frac{V_{phase}}{m_{phase}} = \nu_{phase} \tag{4.12}$$

$$(\frac{m_{phase}}{m_{total}}) = f_{phase} \tag{4.13}$$

$$\nu_{ext} = \frac{V_{total}}{m_{total}} = f_{cryst} \cdot \nu_{cryst} + (1 - f_{cryst}) \cdot \nu_{amorph} \tag{4.14}$$

$$f_{cryst} = \frac{\nu_{exp} - \nu_{amorph}}{\nu_{amorph} - \nu_{cryst}} \tag{4.15}$$

The estimated massive fraction, f_{cryst} can be easily obtained, using a experimental density of $1.145 \frac{g}{cm^3}$ as 0.37.

Chapter 5

Water-Poly−ε−caprolactone

5.0.3 Introduction

Poly-ε-caprolactone (PCL) is an aliphatic poly-ester composed of hexanoate repeat units. At room temperature, PCL is highly soluble in chloroform, dichloromethane, carbon tetrachloride, benzene, toluene, cyclohexanone and 2-nitropropane; slightly soluble in acetone, 2-butanone, ethyl acetate, dimethylformamide and aceto-nitrile; and insoluble in alcohols, petroleum ether, diethyl ether and water. PCL displays the rare property of being miscible with many other polymers (such as poly(vinyl chloride), poly(styrene–acrylonitrile), poly(acrylonitrile butadiene styrene), poly(bisphenol-A) and other polycarbonates, nitrocellulose and cellulose butyrate), and is also mechanically compatible with others (polyethylene, polypropylene, natural rubber, poly- (vinyl acetate), and poly(ethylene–propylene) rubber).

5.1 Molecular mechanics

Starting from the model previous build we can now deal with the solution Water-Poly−ε−caprolactone model.

5.1.1 System definition

A cubic cell of Water-Poly−ε−caprolactone, with a lattice parameter of 50 nm and a concentration of 1.2 ‰, is modeled. The costruction has made by inserting water molecules in the previous equilibrated system. Further, with a force field reported based on CHARMM[32], a dynamic in NPT ensemble is calculated with velocity verlet and integrated through NAMD program.

5.1.2 Equilibration

By analysis of radial distribution function, reported in figure 5.2, we obtained certain about the interaction occurring in the polymer solution. We can established a typical length of hydrogen bonding interaction and a range of length around aspecific interactions occur. Furthermore an specific and aspecific dimer can be drawed by such conclusions.

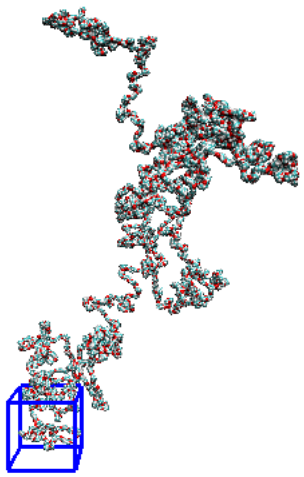

Figure 5.1: Polycaprolactone molecules and its cubic box

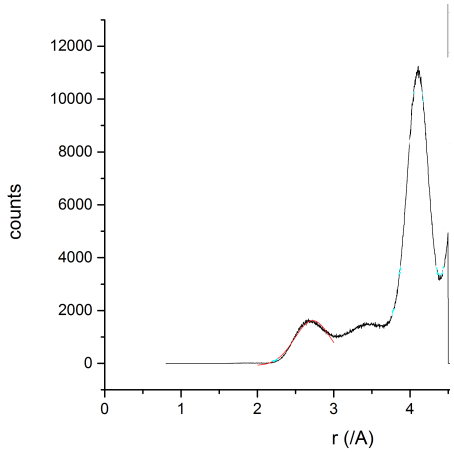

Figure 5.2: Radial distribution function diagram of water hydrogen atoms around the carbonyl oxygen of poly-ε-caprolactone

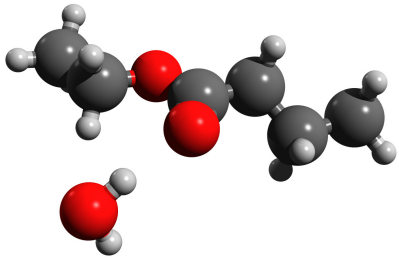

Figure 5.3: Model of water-poly-ε-caprolactone specific-interacting dimer

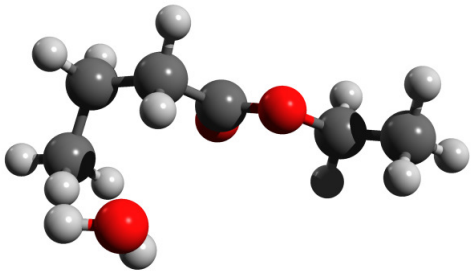

Figure 5.4: Model of water-poly-ε-caprolactone aspecific-interacting dimer

5.2 Ab-initio structures

In order to obtain the equation of state parameters, the specific interactions occurring between the hydrogen bond acceptor group in water and poly-ε-caprolactone and the HB donor group locate, as hydrogen atoms in water molecule, have to be analyzed. One could assume that as long the equilibration time as phase space has been fully exploited. Therefore we could proceed to extract representative structure of specific interactions occurring between penetrant and polymer. A simple *Fortran 90* program is used to extract the structures of interest as they exhibit representative inter-atomic distances. Density functional theory calculations described in chapter 2, following a method also called B3LYP-D2, are used to obtain the total electron energy of extracted dimers. The basis sets used are the double zeta Pople 6-311g**. Structure are analyzed and further optimized with the GAMESS-UK program. Optimizations are carried out to have truly stationary structures where the vibrational analysis can be done. This characteristic allow us to calculate the force matrix acting on each atoms and therefore the frequency related to their normal modes of vibrations.

$$\Delta E = E_{h-bond} - E_{vdw-bond} \tag{5.1}$$

ΔE_{el+vdw}	ΔU	ΔS
-11.22	-11.54	10.51

The value calculated is very similiar of those calculated by the fitting of the experimental PVT data by NRHB equations machinery. The method confirm itself to provide the energy and entropy variations involved in the creation of an hydrogen bond interaction.

5.3 Prediction of specific interactions

Molecular dynamics can be used to investigate the phase space of the model, time evolution of the model used fully reflects the Lagrangian behavior in statistical thermodynamics. It is, also, a valuable tool to find predictive data in material science. As matter of fact the model well describe the system under observation, one can create a lot of algorithms to extrapolate and average data directly from molecular dynamics calculations. To be predictive, on the number of specific *interactions* occurring in the system, beside one have to analyze a large number of configurations with a lot of related computational work. To deal with thermodynamics one have to hardly find a program that analyzes the huge number of configurations required to obtain a statistically significant observable. In fact, we proceeded to write an algorithm that analyzes the atomic groups of interest in the course, and it would calculate the occurrence. Because of the large number of atoms and the number of configurations, the computational cost is usually very high. Therefore we use one of the more advanced ways of calculation. Among these, we choice two aspect to have better performance:

- the reduction of the number of calculated distances to those of only specifically interacting groups through the early exit from the calculation of distances much greater than the required;

- and finally the use of the OpenMP programming technology that allows the *fork* of the high number of multiplications on multiple processors making the strictly speaking parallel computing.

The program is fully reported in the appendix A. The data obtained show that the main part of hydrogen bonds formend in this model occurs because of the interaction between carbonyl oxygen atom of PCL and hydrogen atom of water molecule. It is worth noting that ester oxygen contribute to hydrogen solvatation of water moleculs is trascurable.

ω_{H_2O}	$C=O$	$C-O$	H_2O
0.005	63	17	18
0.0075	75	8	16
0.01	79	1	19

Percentual fraction of h-bond acceptor group as function of ω_{H_2O}, percentual mass water concentration

The results, reported in Figure 5.5, show a not excellent agreement with data if one use little angular tolerance searching the hydrogen-bonds. Typical use of a 0.11 radians tolerance show decrease of the interaction's number, indeed increasing it to 0.33 radians drive a close agreement with experimental data and theory predicted values. This suggest that the Lagrangian equation assumed to be true is not so good. The force that achieved for this behavior is to be found as the coulomb forces that simulated and dictates the hydrogen bonding formation. As matter of fact the coulomb's forces in molecular dynamics are usually assumed to act as summation of potential fields centered on nuclei of the atoms. This is not true in hydrogen bonding as the electron density dictates the fields shape and so on the hydrogen bonding. The lone pairs on oxygen atoms causes severe deviations of the coulomb's fields, leading from a spherical field to a nearly asymmetrical. This behaviour can be taken into considerations introducing a new type of entities in the molecular mechanics model, the pseudo atoms. They, rigid bonded to oxygen atoms, carry the lone pairs charge in a better fashion and influence the total energy no more.

In conclusion the model accurately predict the number and the type of hydrogen bonds in the mixtures. Thus we can argue the efficiency of the molecular dynamics to explore and analize the phase space, to model and to account the description of such materials in terms of mean field and specific interactions too.

5.4 Topology of interactions

Using the atomistic model treated in the previous section we are able, theoretically, to calculate all the physical properties of a bulk of poly-ε-caprolactone-water mixture. This latter kind of mixture, as metioned before, is as of notable importance as implicate in the biodegradation processes. The water position in the lattice, and its modes of interaction are key factors in evaluating its mechanical performance and its chemical resistance to aging. Thus we develop an algorithm to sample the trajectory and found the networks of structures where

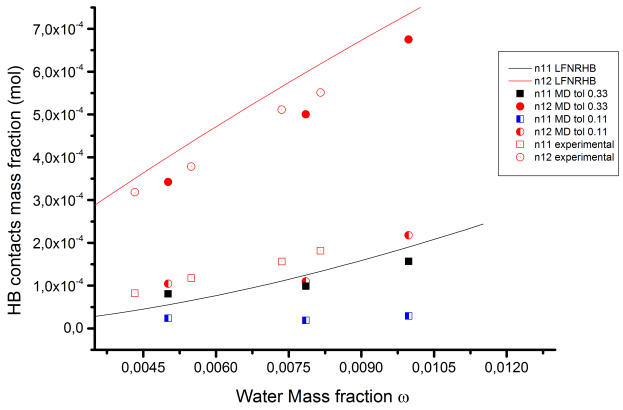

Figure 5.5: Experimental and simulated number of specific interaction occurring in a polycaprolactone-water mixtures. Simulated value are obtained by lattice fluid theory and by molecular dynamics with two angular tolerances, 0.33 and 0.11 radians

hydrogen bond forms. Each frame *frame*, that is timestep structures, are analyzed to find the hydrogen bonds, the result of this calculation are written to a data structure called *hlist*. When the *hlist* is produced a temporal analysis is done. The time variable allow to discriminates what kind of structures can be considered stable and to give a network hierarchy of hydrogen bonds. The hierarchy allow us to do a shell analysis, that is we are now able to find the first hydratation shell of water on PCL and then to find the second shell, the structures of molecules that interact through hydrogen bond with the first shell. The time range, where the persistence of a network structure is evaluated, is much important, we choice to analyze timestep of 1 µs, and consider stable a structure that persists over almost 9 sub-timestep of 0.1µs. The algorithm is reported in the appendix D. The analysis of the developed method is then carried out.

Bond type Looking for known hydrogen bond network Determining the hydrogen bond type

Main HB bond	occurence (‰)
Water PCL	97
Water Water	3

Percentual fraction of occurence of h-bond network structures

Topology Analysis of neighborhoods hydrogen bonds acting as donor or acceptor over the donor molecule of the hydrogen *stable* bond (water molecule) reveal a strong trend of the water molecule to interact with two repeating units at time. These structure are characterized by both hydrogen atoms of one water molecule donating hydrogen bond over two different carbonyl oxygen, resulting

in a sort of *reticulation* between polymer chains. This behavior is consistent with a recent spectroscopic work.[20]

Structure name	n. hb bond	occurence (‰)
Single hydrogen bond	1	17
Bridge Structure	2	67.7
Bridge Str. plus water	3	9.7
Water Water	1	3

Percentual fraction of occurence of h-bond network structures

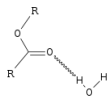

Figure 5.6: Single hydrogen bond: polymer repetition unit and water molecule

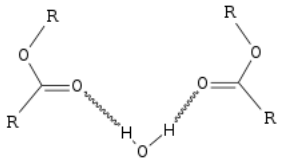

Figure 5.7: Bridge structure: two hb bonds between two polymer repetition units and water molecule

The second shell analysis allow us to recognize an important *sovra*-structure where another water molecule donate hydrogen bond over the previous reported *bridge* structure.

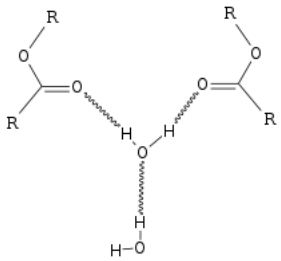

Figure 5.8: Bridge with additional water molecule structure: tree bonds between two polymer repetition units and two water molecules

The analysis of the first shell reveals also negligible fraction of hydrogen bonds between isolated water molecules.

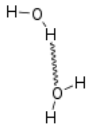

Figure 5.9: Water Water dimer structure: one bonds between two water molecules

5.5 Conclusion

The objective of this thesis has been the development and the analysis of microscopic and macroscopic mathemathical models needed to describe the poly-ε-caprolactone-water polymer mixtures. PCL biodegrades within several months to several years depending on the molecular weight, the degree of crystallinity of the polymer, and the conditions of degradation. Many microbes in nature are able to completely biodegrade PCL. The amorphous phase is degraded first, resulting in an increase in the degree of crystallinity while the molecular weight remains constant. Then, cleavage of ester bonds results in mass loss. The polymer degrades by end chain scission at higher temperatures while it degrades by random chain scission at lower temperatures. PCL degradation is autocatalysed by the carboxylic acids liberated during hydrolysis but it can also be catalysed by enzymes, resulting in faster decomposition. While PCL can be enzymatically degraded in the environment, it cannot be degraded enzymatically in the body. The poly-ε-caprolactone water mixture model represents a mandatory point to describe its behavior in the human body and in enviromental conditions. The starting idea is to use the Non Random Hydrogen Bonding, also known as NRHB, lattice theory to describe and potentially predict the mechanical, physical and chemical properties of the mixture. These lattice theory require a previous work to fit experimental data and to obtain the model parameters. Thus we want to sypply *ab-initio* this parameters. To investigate the dependence of lattice fluid theories from quantum view a previous investigation of thermodynamic parameters, needed to fully describe the mechanical, physical and chemical properties of the mixture, was done. Then starting from the atomistic force field, we build a model able to well describe the phase space of the system. Macroscopic properties are able to be predicted as well as density and radial distribution functions. As we were interested to investigate the relationship between macroscopic conditions and microscopic induced properties by solvent, we use the data provided by molecular dynamics to provide input structures to Density Functional Theory calculations. These latter allow us to optimize and evalute specific interaction structures, to calculate their energy and their thermodynamic parameters. The value calculated is very similiar of those calculated by the fitting of the experimental PVT data by NRHB equations machinery. The method confirm itself to provide the energy and entropy variations involved in the creation of an hydrogen bond interaction. Further an analysis of the trajectory produced by molecular dynamics is done, showing a molecular dynamics model able to reproduce macroscopic and microscopic observables. It is worth noting to carefully model the force field to the observables we want observe. Topology analysis is also done, predicting accurately the kind

of hydrogen bonded *sovra*-structures, giving reason of spectroscopic data about water shell of hydratation.

.1 Fortran77 program to extact dimers DlPOLY trajectory

This program have been written to analyze and extract dimer, with a specific interaction distance from DlPOLY4 trajectory file and write they to an simple xyz file format.

```
4     0program analysis
      implicit none
      integer atn, k, molatm, dimatm, point
      integer*8 keytrj, imcon, megatm, frame, i, aframe, nstep, iatm, j,
     +nmax, ia, ib, aa, ab, t, s
      parameter ( nmax=5000)
      real*8 a(1,3), p, q, tstep, time, weight, charge, rsd, x(nmax,3),
     +v(nmax,3), f(nmax,3), rij, rs, r1, r2, r
      character b, d, e, atmnam(nmax)
      open(1, file='HISTORY', status='old')
      open(2, file='dimer.xyz', status='unknown')
c format character
191   format(a73)
192   format(a1)
101   format(i12)
103   format(a5, 1x, i8, 1x, a5, 1x, i8, 1x, a8, 1x,i6, 1x, i6)
c reading the distance
      write(6,*) 'WHAT IS DIMER INTERACTIONS DISTANCE?'
      read(5,*) r
      r1 = r - 0.005
      r2 = r + 0.005
c reading the molecule atom number
      write(6,*) 'WHAT IS MOLECULAR ATOMIC NUMBER?'
      read(5,*) molatm
c starting index point variable
      point=0
c reading the config file
      read(1,*) d
c     write(2,*) 'HISTORY FILE DIMER ANALYSIS'
      read(1,*) keytrj, imcon, megatm, frame
c     write(2,*) megatm
      do k=1,frame
13      read(1,*) b, nstep, megatm, keytrj, imcon, tstep, time
        if (k.ge.1.and.imcon.le.2) then
c crystal parameter
          read(1,*) a(1,1)
          read(1,*) p, a(1,2)
          read(1,*) p, q, a(1,3)
c fine blocco
c         write(2,*) 'orthorhombic'
c         write(2,*) a
        else
```

```
          read(1,*) p
          read(1,*) p
          read(1,*) p
        endif
c controllo di inizio blocco
c     per ogni frame crea matrice
        do ia=1, megatm
          read(1,*) atmnam(ia), iatm, weight, charge, rsd
          read(1,*) (x(ia,j), j=1,3)
          if (keytrj.ge.1) then
            read(1,*) (v(iatm,j), j=1,3)
            if (keytrj.ge.2) then
              read(1,*) (f(iatm,j), j=1,3)
            endif
          endif
c         write(2,*) atmnam, x(ia,:)
c          write(6,*) atmnam(1:1), x(ia,:)
        end do
        rs= 0.0
        do ia=1, megatm, molatm
          do ib=molatm+1, megatm, molatm
            rs=0.0D0
            do j=1,3
              rs = rs + (x(ia,j) - x(ib,j))*(x(ia,j) - x(ib,j))
            end do
            rij = SQRT(rs)
            if ( rij .lt.r2.and.rij.gt.r1) then
              dimatm = 2 * molatm
              point=point+1
              write(2,101) dimatm
              write(2,103) 'point', point, 'nstep', nstep, 'atmindex',
     +ia, ib
              do t=0, molatm-1
                aa= ia+t
                write(2,*) atmnam(aa), x(aa,:)
              end do
              do s=0, molatm-1
                ab= ib+s
                write(2,*) atmnam(ab), x(ab,:)
              end do
            end if
          end do
        end do
      enddo
      write(6,*) 'JOB COMPLETED'
      close(1)
      close(2)
      stop
      end
```

```
c una function per gli atomi
c       character x
c       if (x.eq.'c') then
c         atn= 6
c       elseif (x.eq.'c') then
c         atn= 6
c       elseif (x.eq.'o') then
c         atn= 8
c       elseif (x.eq.'h') then
c         atn= 1
c       endif
c       return
c       end
```

.2 Topology of PCL-Water solution model

We report the topology used to create the *force field* needed to run molecular dynamics with parameters:

```
*  \\\\\\\ CHARMM36 All−Hydrogen Lipid Topology File ///////
*  All comments and questions should be submitted to the
*  parameter forum at the CHARMM website: www.charmm.org
*
36  1

!NOTE: Reordering of atoms in the choline region of the PC lipids as
!requried for the domain decomposition code in CHARMM. This will not
!change the energies/forces, but PSFs generated with the previous
! lipid toppar files may not work. To overcome this a toppar stream
! file , toppar_all36_lipid_orig_pc_atom_order.str, has been created
!which contains the original atom ordering. August 2012
!

!references
!
!Jeffery B. Klauda, Richard M. Venable, J. Alfredo Freites, Joseph
!W. O'Connor, Douglas J. Tobias, Carlos Mondragon−Ramirez, Igor
!Vorobyov, Alexander D. MacKerell, Jr. and Richard W. Pastor "Update of
!the CHARMM All−Atom Additive Force Field for Lipids: Validation on Six
!Lipid Types" J. Phys. Chem. B 2010, 114, 7830−7843
!

* TOPOLOGY FILE FOR PROTEINS USING EXPLICIT HYDROGEN
    ATOMS: VERSION 19
```

```
*
   20    1                    ! Version number

!references
!Reiher, III ., W.E. Theoretical Studies of Hydrogen Bonding, Ph.D.
!Thesis, Department of Chemistry, Harvard University, Cambridge, MA,
!USA, 1985
!
!and
!
!Neria, E., Fischer, S., and Karplus, M. Simulation of Activation Free
!Energies in Molecular Systems, Journal of Chemical Physics, 1996, 105:
!1902−21.


! SOLVENT ZONE

DEFA FIRS NONE LAST NONE
AUTO ANGLES DIHE

RESI HOH        0.000 ! tip3p water model, generate using noangle
     nodihedral
GROUP
ATOM H1 HT     0.417
ATOM O OT     −0.834
ATOM H2 HT     0.417
!BOND O H1 O H2 H1 H2 ! the last bond is needed for shake
BOND O H1 O   H2
ANGLE H1 O H2           ! required
ACCEPTOR O
PATCHING FIRS NONE LAST NONE


! POLYMER ZONE

DEFA FIRS NONE LAST NONE
AUTO ANGLES DIHE

! POLYCAPROLACTAME ZONE

RESI C6H 0.00 ! Pcl residue
GROUP
ATOM C1 CTL2 0.08
ATOM H1 HAL2 −0.09
ATOM C2 CTL2 −0.18
ATOM H2 HAL2 −0.09
ATOM H3 HAL2 0.09
ATOM C3 CTL2 −0.18
ATOM H4 HAL2 0.09
ATOM H5 HAL2 0.09
```

```
ATOM C4 CTL2 −0.18
ATOM H6 HAL2 0.09
ATOM H7 HAL2 0.09
ATOM C5 CTL2 −0.22
ATOM H8 HAL2 0.09
ATOM H9 HAL2 0.09
ATOM C6 CL    0.90
ATOM H10 HAL2 0.09
ATOM O1 OSL −0.49
ATOM O2 OBL −0.63
BOND C1 H1 C1 H2 C1 C2
BOND C2 H3 C2 H4 C2 C3
BOND C3 H5 C3 H6 C3 C4
BOND C4 H7 C4 H8 C4 C5
BOND C5 H9 C5 H10 C5 C6
BOND C6 O1
```

.3 Hlih program to analyze trajectory to find HB statistics

This is the program to analyze the trajectory exported in a pdb file and find the hydrogen bond wanted in a OpenMP programming.

```
program phlo2

 use iso_c_binding
 use omp_lib
 use constant
 use modh

 implicit none

      character*8 :: rehlis,response
      character*4 :: donor(30),acceptor(30)
      character*3 :: resdon(30),resacc(30)
      character*4,allocatable :: atname(:)
      character*3,allocatable :: resname(:)
      character*2,allocatable :: element(:),charge(:)
      character,allocatable :: altloc(:),chainid(:),icode(:)

      integer :: i,j,molatm,frame,tstep,step,maxfra, stste, enste, &
            maxste,totdon,totacc,nhbdt,nhbat,per(2),tsc,stamp,hbond
      integer,allocatable :: serial (:),resseq(:), dlist (:,:) , alist (:,:) , hlist
          (:,:,:)

      real :: a(3),a2(3),rcut(4),drayco(30),arayco(30),dangle(30),&
            aangle(30),dst,angle,p(3),q(3),r(3),tolang
      real,allocatable :: px (:,:) ,tempf(:),occ(:)
```

```
      real,allocatable :: fx (:,:)
      logical  :: io

!       open(unit=2, file='frame.pdb', status='unknown')
      open(unit=3, file='inputm', status='old')
!       open(unit=4, file='phlista ', status='new')

104   format(A8)
105   format(A4,1X,A3,1x,f5.2,1x,f5.2)
106   format(f3.2,1X,f3.2,1X,f3.2,1X,f3.2)

! READING THE INPUT

read(3,*) response, stamp
read(3,*) molatm
read(3,*) tstep
read(3,*) maxfra
read(3,*) stste , enste

if (response.eq.'FRAMEWOP') then
frame=stamp
goto 201
endif

read(3,106) rcut(:)
read(3,*) tolang
read(3,*) tsc

nhbdt=0
nhbat=0
donor(:)=''
resdon(:)=''
resacc (:)=''
acceptor(:)=''

203 read(3,104) rehlis
if ( rehlis .eq.'DONOR␣␣␣') goto 204
if ( rehlis .eq.'ACCEPTOR') goto 205
if ( rehlis .eq.'END␣␣␣␣␣') goto 201
204 do i=1,30
read(3,105) donor(i),resdon(i),drayco(i),dangle(i)
dangle(i)=dangle(i)/180
if (donor(i).eq.'END␣') GOTO 203
nhbdt=nhbdt+1
end do
205 do j=1,30
read(3,105) acceptor(j),resacc(j),arayco(j),aangle(j)
aangle(j)=aangle(j)/180
if (acceptor(j).eq.'END␣') goto 203
nhbat=nhbat+1
```

```
end do

! ACCESSORY VARIABLE

201 continue

per(:)=0
maxste=maxfra/tstep

! READING THE PDB FRAME

allocate(serial(molatm),atname(molatm),altloc(molatm),fx(molatm,3),
    &
              resname(molatm),chainid(molatm),resseq(molatm),icode(
                  molatm),&
              px(molatm,3),occ(molatm),tempf(molatm), &
              element(molatm),charge(molatm))

allocate(hlist(maxste,molatm/4,2))

! Auxiliary VARIABLE

hlist(:,:,:)=0
per(2)=0
step=0

do frame=stste,enste,tstep
step=step+1

!step=(frame-stste)/tstep

! PERCENTUAL COMPLETED

!per(1)=(step*100/(maxste+1))
!if (per(1).gt.per(2)) then
!per(2)=per(1)
!write(6,*) 'COMPLETED', per(1)
!end if

! Auxiliary VARIABLE
hbond=0

if (step.eq.1) io=.true.

call readx2(frame,io,molatm,px,atname,resseq,resname,serial,chainid,a)
call px2fx(a,molatm,px,fx)


if (io.eqv..true.) then
```

```
io =.false.

! call writepdb(molatm,px,atname,resseq,resname,serial,chainid,a)

! LOCALTE THE DONOR AND ACCEPTOR GROUP

allocate(dlist(molatm,3),alist(molatm,3))
totdon=0
totacc=0

do j=1,nhbdt
do i=1,molatm
      if (atname(i).eq.donor(j).and.resname(i).eq.resdon(j)) then
        totdon=totdon+1
        dlist(totdon,1)=serial(i)
        dlist(totdon,3)=j
end if
end do
end do

do j=1,nhbat
do i=1,molatm
      if  (atname(i).eq.acceptor(j).and.resname(i).eq.resacc(j)) then
        totacc=totacc+1
        alist(totacc,1)=serial(i)
        alist(totacc,3)=j
end if
end do
end do

! Locating specif interagent group neightbordhood atom

do i=1,3
  a2(i)=a(i)**2
end do

do i=1,totdon
  do j=1,molatm
    call prij(dlist(i,1),j,a2,fx,dst)
    if (dst.lt.drayco(dlist(i,3)).and.dst.gt.0.5)   dlist(i,2)=j
  end do
end do

do i=1,totacc
  do j=1,molatm
    call prij(alist(i,1),j,a2,fx,dst)
    if (dst.lt.arayco(alist(i,3)).and.dst.gt.0.5)  alist(i,2)=j
  end do
end do
```

```
! ENDING FIRST FRAME ANALYSIS

end if

!  FIND A HYDROGEN BOND

do i=1,3
  a2(i)=a(i)**2
end do

!$omp parallel do collapse(2) private(p,q,r,angle,dst) schedule(dynamic)
do i=1,totdon
  do j=1,totacc
   call prij(dlist(i,1),alist(j,1),a2,fx,dst)
   if (dst.gt.rcut(1).and.dst.lt.rcut(2)) then
     p(:)=fx(alist(j,1),:)
     q(:)=fx(dlist(i,1),:)
     r(:)=fx(alist(j,2),:)
     call pangle(p,q,r,a2,angle)
     if (angle.lt.aangle(alist(j,3))+tolang.and.angle.gt.aangle(alist(j,3))
         -tolang) then
       !$omp critical
       hbond=hbond+1
       hlist(step,hbond,1)=dlist(i,1)
       hlist(step,hbond,2)=alist(j,1)
       !$omp end critical
     end if
   end if
  end do
end do
!$omp end parallel do

! WRITING HLIST FILE OF HYDROGEN BOND FOUND IN
    TRAIECTORY
  write(6,*) step, hbond
do i=1,hbond
  write(6,*) hlist(step,i,:)
end do

! END OF STEP

end do

deallocate(serial,atname,altloc,resname,chainid,resseq,icode,occ,tempf,
    element,charge)
deallocate(dlist, alist )
deallocate(hlist)

close(2)
close(3)
```

```
stop
end
```

```
module constant
! Declare local constant Pi
REAL, PARAMETER :: Pi = 3.1415927
end module constant

module modh
contains

subroutine readx(frame,molatm,px,atname,resseq,resname,serial,chainid,a)
      character*93 :: dummy
      character*6 :: recnam
      character*4,allocatable :: atname(:)
      character*3,allocatable :: resname(:)
      character*2,allocatable :: element(:),charge(:)
      character,allocatable :: altloc(:),chainid(:),icode(:)
      integer :: io,i,molatm,frame2,frame
      integer,allocatable :: serial(:),resseq(:)
      real :: a(3),pangle(3),b(3,2)
      real,allocatable :: px(:,:),tempf(:),occ(:)
      open(unit=1, file='traj.pdb', status='old')
      open(unit=9, file='fort.xst', status='old')
101   format(A6,I5,1X,A4,A1,A3,1X,A1,I4,A1,3x,f8.3,f8.3,f8.3,f6.2,f6.2,10X,
     A2,A2)
!     Skip lines
      read(9,*) dummy
      read(9,*) dummy
      read(1,*) recnam,a(1),a(2),a(3),pangle(1),pangle(2),pangle(3)
!     Reaching a frame
200   read(9,*) frame2, a(1),b(1,1),b(1,2),b(2,1),a(2),b(2,2),b(3,1),b(3,2),
     a(3)
      if (frame2.ne.frame) then
      do i=1,molatm+1
      read(1,*) dummy
      end do
      goto 200
      endif
allocate(altloc(molatm),icode(molatm),occ(molatm),tempf(molatm), &
              element(molatm),charge(molatm))
      do i=1,molatm
      read(1,101,iostat=io) recnam,serial(i),atname(i),altloc(i),resname(i),
            &
              chainid(i),resseq(i),icode(i),px(i,1),px(i,2),px(i,3),occ(i),
                  tempf(i),&
              element(i),charge(i)
      if (recnam=='END␣␣␣') exit
```

```
      end do
close(1)
close(9)
end subroutine readx

subroutine readx2(frame,io,molatm,px,atname,resseq,resname,serial,chainid,a
    )
      character*93 :: dummy
      character*6 :: recnam
      character*4,allocatable :: atname(:)
      character*3,allocatable :: resname(:)
      character*2,allocatable :: element(:),charge(:)
      character,allocatable :: altloc(:),chainid(:),icode(:)
      integer :: j,i,molatm,frame2,frame
      integer,allocatable :: serial(:),resseq(:)
      logical :: io
      real :: a(3),pangle(3),b(3,2)
      real,allocatable :: px(:,:),tempf(:),occ(:)
101   format(A6,I5,1X,A4,A1,A3,1X,A1,I4,A1,3x,f8.3,f8.3,f8.3,f6.2,f6.2,10X,
    A2,A2)

      if (io.eqv..true.) then
      open(unit=1, file='traj.pdb', status='old')
      open(unit=9, file='fort.xst', status='old')
!     Skip lines
      read(9,*) dummy
      read(9,*) dummy
      read(1,*) recnam,a(1),a(2),a(3),pangle(1),pangle(2),pangle(3)
      endif

!     Reaching a frame
200   read(9,*) frame2, a(1),b(1,1),b(1,2),b(2,1),a(2),b(2,2),b(3,1),b(3,2),
    a(3)
      if (frame2.ne.frame) goto 200

allocate(altloc(molatm),icode(molatm),occ(molatm),tempf(molatm), &
              element(molatm),charge(molatm))
      do i=1,molatm
      read(1,101,iostat=j) recnam,serial(i),atname(i),altloc(i),resname(i),
           &
              chainid(i),resseq(i),icode(i),px(i,1),px(i,2),px(i,3),occ(i),
                   tempf(i),&
              element(i),charge(i)
      if (recnam=='END␣␣␣') exit
      end do
end subroutine readx2


subroutine writepdb(molatm,px,atname,resseq,resname,serial,chainid,a)
      character*4,allocatable :: atname(:)
```

```
      character*3,allocatable :: resname(:)
      character,allocatable :: chainid(:)
      integer :: io,i,molatm
      integer,allocatable :: serial(:),resseq(:)
      real :: a(3)
      real,allocatable :: px(:,:)
      open(unit=5, file='frame0.pdb', status='new')
101   format('ATOM  ',I5,1X,A4,1X,A3,1X,A1,I4,4x,f8.3,f8.3,f8.3)
102   format('CRYSTA',f6.3,1x,f6.3,1x,f6.3)
      write(1,102) a(1),a(2),a(3)
      do i=1,molatm
      write(5,101,iostat=io) serial(i),atname(i),resname(i),   &
            chainid(i),resseq(i),px(i,1),px(i,2),px(i,3)
      end do
close(5)
end subroutine writepdb



subroutine px2fx(a,molatm,px,fx)
integer :: i,j,molatm
real :: a(3),px(molatm,3),fx(molatm,3)
do i=1,molatm
 do j=1,3
  fx(i,j)=px(i,j)/a(j)
  fx(i,j)=fx(i,j)-anint(fx(i,j))
 end do
end do
end subroutine px2fx

subroutine prij(don1,acc2,a2,fx,dst)
integer :: i,don1,acc2
real :: a2(3), dist(4),dst
real,allocatable :: fx(:,:)
dist(:)=0
dst=0
do i=1,3
 dist(i)=fx(don1,i)-fx(acc2,i)
 dist(i)=dist(i)-anint(dist(i))
 if (abs(dist(i)).gt.0.25) then
   dst=0
   goto 12
 endif
 dist(4)=dist(4)+dist(i)**2*a2(i)
end do
dst=sqrt(dist(4))
12 continue
end subroutine prij

subroutine pangle(p,q,r,a2,angle)
```

```
real :: angle,mud(6),p(3),q(3),r(3),a2(3)
mud(:)=0
do i=1,3
mud(1)=r(i)−p(i)
mud(2)=(mud(1)−anint(mud(1)))**2*a2(i)
mud(1)=q(i)−p(i)
mud(3)=(mud(1)−anint(mud(1)))**2*a2(i)
mud(4)=mud(4)+mud(2)*mud(3)
mud(5)=mud(5)+mud(2)
mud(6)=mud(6)+mud(3)
end do
do i=4,6
mud(i)=sqrt(mud(i))
end do
angle=acos(mud(4)/(mud(5)*(mud(6))))
if (angle.gt.1) angle=angle−1
end subroutine pangle

end module modh
```

.4 Hmens program to analyze trajectory to find HB network structures

This is the program to analyze the trajectory exported in a pdb file and find the network hydrogen bond structures Fortran90 programming.

```
program hmens
      ! version 5.3 written in naples 30 semptember 2015
      implicit none

      logical :: success
      character*93 :: dummy
      character*73 :: title
      character*8 :: rehlis
      character*6 :: recnam
      character*4 :: donor(30),acceptor(30)
      character*3 :: resdon(30),resacc(30),dne,response
      character*4,allocatable :: atname(:),clustn(:)
      character*3,allocatable :: resname(:),resmol(:)
      character*2,allocatable :: element(:),charge(:)
      character,allocatable :: altloc(:),chainid(:),icode(:)

      integer :: io,i,j,k,l,m,n,o,p,molatm,frame,tstep,step,st2fr,pulse,
     pu2fr,maxfra,&
          maxste,totdon,totacc,nhbdt,nhbat,hcount,per(2),tsc,indez(2),
               stamp,&
          ncvlu,bond,molecule,nmol,hbo,fmolt,hstru(70,70),nam(70),score
      integer,allocatable :: serial(:),resseq(:),dlist(:,:),alist(:,:),hlist
     (:,:,:),&
          hbond(:),sbond(:,:),smol(:,:),clusts(:),&
          hbondi(:,:),hblis(:,:)

      real :: a(3),pangle(3),a2(3),rcut(4),distmi(3),distma(3),b(3,2),&
          raya,rayb,clustss,repro(49,2)
      real,allocatable :: px(:,:),tempf(:),occ(:),hdist(:,:)
      real,allocatable :: fx(:,:),ppx(:,:),rij(:,:,:),clust(:,:),irstru
     (:,:,:)


      open(unit=1, file='traj.pdb', status='old')
      open(unit=2, file='frame053.pdb', status='new')
      open(unit=3, file='input', status='old')
      open(unit=4, file='distance5', status='new')
      open(unit=9, file='fort.xst', status='old')
!     open(unit=7, file='clust.xyz', status='new')
      open(unit=8, file='hbond5', status='new')
!     open(unit=10, file='RAYCOV', status='old')
      open(unit=11, file='probability5', status='new')
```

```
101   format(A6,I5,1X,A4,A1,A3,1X,A1,I4,A1,3x,f8.3,f8.3,f8.3,f6.2,f6.2,10X,
      A2,A2)
102   format('CRYST1',f9.3,f9.3,f9.3,f7.2,f7.2,f7.2,1X,'P1␣␣␣␣␣␣␣␣',4X)
103   format('END')
104   format(A8)
105   format(A4,1X,A3)
106   format(f3.2,1X,f3.2,1X,f3.2,1X,f3.2)
107   format(A6,23x,f8.3,f8.3,f8.3,26x)
108   format(A9,1x,I3,1x,'%')
109   format(A73)
110   format(A2,1x,f10.6,1x,f10.6,1x,f10.6)
111   format(A3)
!   step a_x a_y a_z b_x b_y b_z c_x c_y c_z o_x o_y o_z s_x s_y s_z
      s_u s_v s_w

! READING THE INPUT

read(3,*) molatm
read(3,*) tstep
read(3,*) maxfra
!write(6,*) 'do you want a structure?'
response='no␣'
!if (response.eq.'yes') read(3,*) stamp
read(3,106) rcut(:)
read(3,*) tsc

! ACCESSORY VARIABLE

per(:)=0
maxste=maxfra/tstep
step=1

! READING THE PDB FRAME

!skip
      read(9,*) title
      read(9,*) title
! reading cell frame
      read(9,*) frame

      read(1,*) recnam,a(1),a(2),a(3),pangle(1),pangle(2),pangle(3)

allocate(serial(molatm),atname(molatm),altloc(molatm),              &
               resname(molatm),chainid(molatm),resseq(molatm),icode(
                    molatm),&
               px(molatm,3),occ(molatm),tempf(molatm), &
               element(molatm),charge(molatm))

      do i=1,molatm
      read(1,101,iostat=io) recnam,serial(i),atname(i),altloc(i),resname(i),
```

```
            &
              chainid(i),resseq(i),icode(i),px(i,1),px(i,2),px(i,3),occ(i),
                   tempf(i),&
              element(i),charge(i)
       if (recnam=='END␣␣␣') exit
       end do

       read(1,111) dne
       if (dne.ne.'END') stop

allocate(fx(molatm,3))

!write(4,*) per, frame, step, a(:), molatm, tstep, hcut(:)

! WRITE THE IMAGE OF UNITY BOX

207  do i=1,molatm
     do j=1,3
     fx(i,j)=(px(i,j)/a(j))
     end do
     end do

deallocate(px)

     if(step.eq.stamp) goto 216
    if (step.gt.1) goto 214
216 continue

allocate(ppx(molatm,3))

! PDB IMAGE WRITE PART

217  write(2,102) a(:),pangle(:)
     recnam='ATOM␣␣'

     do i=1,molatm
     do j=1,3
     ppx(i,j)=fx(i,j)*a(j)-a(j)*anint(fx(i,j)/a(j))
     end do
     write(2,101,iostat=io) recnam,serial(i),atname(i),altloc(i),resname(i),
          &
              chainid(i),resseq(i),icode(i),ppx(i,1),ppx(i,2),ppx(i,3),occ(i
                   ),tempf(i),&
              element(i),charge(i)
     end do

   deallocate(ppx)
     if(step.eq.stamp) goto 214

! To BE TESTED !!!
```

```
! REALLY

! CALCULATE THE DISTANCE

! SELECT THE INTEREST ATOM PAIR

nhbdt=0
nhbat=0
donor(:)=''
resdon(:)=''
resacc(:)=''
acceptor(:)=''

203 read(3,104) rehlis
write(4,104) rehlis
 if (rehlis.eq.'DONOR␣␣␣') goto 204
 if (rehlis.eq.'ACCEPTOR') goto 205
204 do i=1,30
read(3,105) donor(i),resdon(i)
 if (donor(i).eq.'END␣') GOTO 203
write(4,105) donor(i),resdon(i)
nhbdt=nhbdt+1
end do
205 do j=1,30
read(3,105) acceptor(j),resacc(j)
 if (acceptor(j).eq.'END␣') EXIT
write(4,105) acceptor(j),resacc(j)
nhbat=nhbat+1
end do

! LOCALTE THE DONOR AND ACCEPTOR GROUP
! TESTED

allocate(dlist(molatm,2),alist(molatm,2))
totdon=0
totacc=0

do j=1,nhbdt
do i=1,molatm
       if (atname(i).eq.donor(j).and.resname(i).eq.resdon(j)) then
         totdon=totdon+1
          dlist(totdon,1)=serial(i)
end if
end do
end do

do j=1,nhbat
do i=1,molatm
       if  (atname(i).eq.acceptor(j).and.resname(i).eq.resacc(j)) then
         totacc=totacc+1
```

```
          alist (totacc,1)=serial(i)
end if
end do
end do

! CALCULATE THE SQUARE OF CELL PARAMENTER

214 continue

do i=1,3
a2(i)=a(i)*a(i)
end do

if (step.gt.1) goto 208

! INITIALIZE THE MATRIX OF DISTANCE OF INT H-BOND

allocate(rij(totdon,totacc,5), hlist ((totacc*totdon)/2,3,maxste),hdist((
    totacc*totdon)/2,maxste),hbond(maxste))

208 rij (:,:,:) =0
hbond(step)=0

do j=1,totacc
do i=1,totdon

do k=1,3
    rij(i,j,k)=fx(dlist(i,1),k)-fx(alist(j,1),k)
    rij(i,j,k)=rij(i,j,k)-anint(rij(i,j,k))
    rij(i,j,4)=rij(i,j,4)+rij(i,j,k)*rij(i,j,k)*a2(k)
  end do

! LIKE TAMMURRIATA SONG THIS IS THE THIRdH

  rij(i,j,5)=SQRT(rij(i,j,4))
!write(4,*) atname(alist(j)), alist(j), atname(dlist(i)), dlist(i), rij(i,j
    ,5)
  if (rij(i,j,5).gt.rcut(1).and.rij(i,j,5).lt.rcut(2)) then
          if (resseq(dlist(i,1)).eq.resseq(alist(j,1))) goto 212
          hbond(step)=hbond(step)+1
          hlist(hbond(step),1,step)=dlist(i,1)
          hlist(hbond(step),2,step)=alist(j,1)
          hlist(hbond(step),3,step)=step
          hdist(hbond(step),step)=rij(i,j,5)
  end if
212 continue
end do
end do

!! TESTED
```

```
!
!! TEST WRITING THE DISTANCE

write(4,*) frame,  hbond(step), step

! if  (step.ne.stamp) goto 211
do i=1,hbond(step)
  write(4,*) atname(hlist(i,2,step)), serial ( hlist (i,2,step)),resname(hlist(i
       ,2,step)),&
  atname(hlist(i,1,step)), serial ( hlist (i,1,step)),resname(hlist(i,1,step)),&
  hdist(i,step),  hcount
end do

! READING THE NEXT FRAME
! CONTROL PART

allocate(px(molatm,3))

211 continue

213   read(9,*) frame, a(1),b(1,1),b(1,2),b(2,1),a(2),b(2,2),b(3,1),b(3,2),a
     (3)

      do i=1,molatm
      read(1,101,iostat=io) recnam,serial(i),atname(i),altloc(i),resname(i),
           &
             chainid(i),resseq(i),icode(i),px(i,1),px(i,2),px(i,3),occ(i),
                  tempf(i),&
             element(i),charge(i)
      if (io.ne.0) goto 209
      if (recnam=='END   ') exit
      end do
      if (response.eq.'yes') then
      if (frame.eq.stamp*tstep) goto 209
      end if
! if  (frame.eq.maxfra) goto 218
      read(1,111) dne
      if (dne.ne.'END') STOP
!     TESTING PART
!     I'm BORED to TEST
!     I TEST THIS IN FRAME0 file OUTPUT

218 continue

      per(1)=(frame*100)/maxfra
      if (per(2).lt.per(1)) then
      per(2)=per(1)
      write(6,108) 'COMPLETED',per(2)
      end if
```

```
step=step+1
if (frame.eq.maxfra) goto 209
goto 207

!210 do i=1,molatm+1
!read(1,109)  title
!end do
!read(9,*)  title
!goto vaffanculo

209 continue
deallocate(rij,fx,px, dlist , alist )

do i=1,step-1
write(8,*)  i , hbond(i)
  do j=1,hbond(i)
    do l=1,2
      write(8,*) hlist (j ,l , i)
    end do
  end do
end do

close(1)
close(2)
close(4)
close(9)
close(8)

if (response.eq.'yes') goto 219

write(6,*) 'ANALISYS OF TRAJECTORY COMPLETED'
write(11,*) 'MAKING THE STATISTIC ANALISYS'

open(unit=1, file='traj.pdb', status='old')
open(unit=9, file='fort.xst', status='old')

read(3,*) clustss
ncvlu=0


allocate(hbondi(frame,49))
hbondi (:,:) =0

per(2)=0
   write(6,*) 'ANALISYS COMPLETED',per(2), '%'

 do i=1,maxste-10,10

allocate( rij (molatm,molatm,5),fx(molatm,3),px(molatm,3))
 rij  (:,:,:) =0
```

```
    per(1)=(i*100)/maxste
    if (per(2).lt.per(1)) then
    per(2)=per(1)
    write(6,*) 'ANALISYS COMPLETED',per(2), '%'
    end if

   do j=1,hbond(i)

     hcount=0
     do k=i+1,i+10
     if (k.gt.maxste) exit
       do l=1,hbond(k)
         if ( hlist (j ,1, i ).eq. hlist (l ,1, k).and.hlist(j ,2, i ).eq. hlist (l ,2, k))
             then
         hcount=hcount+1
         end if
       end do
     end do
     if (hcount.ge.tsc) then

     ncvlu=ncvlu+1
     hbondi(ncvlu,1)=1

!     write(8,*) atname(hlist(j,2, i)), serial ( hlist (j,2, i)),resname(hlist(j,2,
      i)),&
!          atname(hlist(j,1, i)), serial ( hlist (j,1, i)),resname(hlist(j,1, i)),&
!          hdist(j, i), hlist (j,3, i), i

     if (i*tstep.eq.frame) goto 215
     if (ncvlu.ne.1) goto 229

!/load fx

px (:,:) =0
fx (:,:) =0

    read(1,109) title
    read(9,*) title
    read(9,*) title

  do m=1,i
    do l=1,molatm+1
    read(1,109) title
    end do
    read(9,*) title
  end do

229 continue
  read(9,*) frame, a(1),b(1,1),b(1,2),b(2,1),a(2),b(2,2),b(3,1),b(3,2),a(3)
```

```
if (frame.ne.i*tstep) then
        do l=1,molatm+1
        read(1,109) title
        end do
        goto 229
endif

do m=1,molatm
   read(1,101,iostat=io) recnam,serial(m),atname(m),altloc(m),resname(m),
       &
              chainid(m),resseq(m),icode(m),px(m,1),px(m,2),px(m,3),occ(m)
                  ,tempf(m),&
              element(m),charge(m)
   if (recnam=='END   ') exit
 end do
  read(1,109) title

 do m=1,molatm
   do n=1,3
   fx(m,n)=(px(m,n)/a(n))
   end do
 end do



 do l=1,3
 a2(l)=a(l)*a(l)
 end do

215 rij (:,:,:) =0
allocate(clustn(molatm),clust(molatm,3),clusts(molatm))
indez(1)=0
do m=1,molatm

do k=1,3
     rij(m,hlist(j,2,i),k)=fx(m,k)-fx(hlist(j,2,i),k)
     rij(m,hlist(j,2,i),k)=rij(m,hlist(j,2,i),k)-anint(rij(m,hlist(j,2,i),k))
     rij(m,hlist(j,2,i),4)=rij(m,hlist(j,2,i),4)+rij(m,hlist(j,2,i),k)*rij(m,
          hlist(j,2,i),k)*a2(k)
end do

  rij(m,hlist(j,2,i),5)=SQRT(rij(m,hlist(j,2,i),4))
  if (rij(m,hlist(j,2,i),5).lt.clustss) then
      indez(1)=indez(1)+1
      clustn(indez(1))=atname(m)
      clusts(indez(1))=serial(m)
      do n=1,3
      clust(indez(1),n)=rij(m,hlist(j,2,i),n)*a(n)
!write(6,*)        clust(indez(1),:)
      end do
  end if
```

```
end do


! Calculate mutual atom distance in the cluster
!

allocate( dlist (indez(1),2) , alist (indez(1),2) )
totdon=0
totacc=0

do m=1,nhbdt
do l=1,indez(1)
        if (atname(clusts(l)).eq.donor(m).and.resname(clusts(l)).eq.resdon(m
            )) then
          totdon=totdon+1
          dlist (totdon,1)=clusts(l)
          dlist (totdon,2)=l
end if
end do
end do

do m=1,nhbat
do l=1,indez(1)
        if   (atname(clusts(l)).eq.acceptor(m).and.resname(clusts(l)).eq.resacc
             (m)) then
          totacc=totacc+1
          alist (totacc,1)=clusts(l)
          alist (totacc,2)=l
end if
end do
end do

allocate(irstru(molatm,molatm,5),hblis(indez(1),2))

hbo=0
hblis (:,:) =0
irstru  (:,:,:) =0

do l=1,totdon
  do m=1,totacc
     if (resseq( dlist (l,1)).eq.resseq( alist (m,1))) exit
     do k=1,3
        irstru ( dlist (l,1) , alist (m,1),k)=clust( dlist (l,2) ,k)−clust( alist (m,2),k
             )
        irstru ( dlist (l,1) , alist (m,1),4)=irstru( dlist (l,1) , alist (m,1),4)&
                  +irstru( dlist (l,1) , alist (m,1),k)∗irstru ( dlist (l,1) , alist (m,1),
                       k)
     end do
     irstru ( dlist (l,1) , alist (m,1),5)=sqrt(irstru( dlist (l,1) , alist (m,1),4))
     irstru ( alist (m,1), dlist (l,1) ,5)=irstru( dlist (l,1) , alist (m,1),5)
```

```
      if (irstru(dlist(l,1),alist(m,1),5).gt.rcut(3).and.irstru(dlist(l,1),
           alist(m,1),5)&
      .lt.rcut(4)) then
!write(6,*) irstru(dlist(l,1),alist(m,1),5), atname(dlist(l,1)),atname(alist
      (m,1))
      hbo=hbo+1
      hblis(hbo,1)=dlist(l,1)
      hblis(hbo,2)=alist(m,1)
      endif
    end do
  end do

! HAVE TO FIND THE MOLECULE

hstru(:,:) =0
nam(:)=0

do l=1,indez(1)
   if (resseq(clusts(l)).eq.resseq(hlist(j,1,i))) then
            nam(1)=nam(1)+1
            hstru(1,nam(1))=clusts(l)
   elseif (resseq(clusts(l)).eq.resseq(hlist(j,2,i))) then
            nam(2)=nam(2)+1
            hstru(2,nam(2))=clusts(l)
   endif
end do

molecule=2

if (resname(hstru(2,1)).eq.'HOH') then
    hbondi(ncvlu,37)=1
    goto 230
endif

!       ,*) hbo,nam(1),l,nam(2)
!     lly tested
! find the first interaction shell

do l=1,nam(1)
   do m=1,hbo
   if (hblis(m,1).eq.hstru(1,l)) then
            do o=2,molecule
             do p=1,nam(o)
              if (resseq(hblis(m,2)).eq.resseq(hstru(o,p))) goto 227
             end do
            end do
    molecule=molecule+1
      if (resname(hblis(m,2)).eq.'HOH') then
         if (atname(hblis(m,2)).eq.'␣O␣␣') hbondi(ncvlu,3)=hbondi(ncvlu,3)
             +1
```

```
          if (atname(hblis(m,1)).eq.'␣O␣␣') hbondi(ncvlu,4)=hbondi(ncvlu,4)
              +1
       endif
        if (resname(hblis(m,2)).eq.'C6H') hbondi(ncvlu,2)=hbondi(ncvlu,2)+1
      do n=1,indez(1)
         if (resseq(clusts(n)).eq.resseq(hblis(m,2))) then
           nam(molecule)=nam(molecule)+1
           hstru(molecule,nam(molecule))=clusts(n)
         endif
      end do
    elseif (hblis(m,2).eq.hstru(1,l)) then
           do o=2,molecule
            do p=1,nam(o)
              if (resseq(hblis(m,1)).eq.resseq(hstru(o,p))) goto 227
            end do
           end do
      molecule=molecule+1
        if (resname(hblis(m,1)).eq.'HOH') then
           if (atname(hblis(m,1)).eq.'␣O␣␣') hbondi(ncvlu,3)=hbondi(ncvlu,3)
               +1
           if (atname(hblis(m,2)).eq.'␣O␣␣') hbondi(ncvlu,4)=hbondi(ncvlu,4)
               +1
        endif
        if (resname(hblis(m,1)).eq.'C6H') hbondi(ncvlu,2)=hbondi(ncvlu,2)+1
      do n=1,indez(1)
         if (resseq(clusts(n)).eq.resseq(hblis(m,1))) then
           nam(molecule)=nam(molecule)+1
           hstru(molecule,nam(molecule))=clusts(n)
         endif
      end do
    endif
227 continue
 end do
end do

fmolt=molecule

do m=1,hbo
 do o=3,fmolt
 do l=1,nam(o)
  if (hblis(m,1).eq.hstru(o,l)) then
           do n=1,molecule
            do p=1,nam(n)
             if (resseq(hblis(m,2)).eq.resseq(hstru(n,p))) goto 228
            end do
           end do
    molecule=molecule+1
           if (resname(hblis(m,2)).eq.'HOH'.and.resname(hstru(o,l)).eq.'C6H'
               ) goto 228
           if (resname(hblis(m,2)).eq.'HOH'.and.resname(hstru(o,l)).eq.'HOH
```

```
                ') &
                    hbondi(ncvlu,6)=hbondi(ncvlu,6)+1
          if (resname(hblis(m,2)).eq.'C6H'.and.resname(hstru(o,l)).eq.'HOH'
                ) hbondi(ncvlu,5)&
                    =hbondi(ncvlu,5)+1
    do n=1,indez(1)
       if (resseq(clusts(n)).eq.resseq(hblis(m,2))) then
          nam(molecule)=nam(molecule)+1
          hstru(molecule,nam(molecule))=clusts(n)
       endif
    end do

  elseif (hblis(m,2).eq.hstru(o,l)) then
          do n=1,molecule
           do p=1,nam(n)
            if (resseq(hblis(m,1)).eq.resseq(hstru(n,p))) goto 228
           end do
          end do
    molecule=molecule+1
          if (resname(hblis(m,1)).eq.'HOH'.and.resname(hstru(o,l)).eq.'C6H'
              ) goto 228
          if (resname(hblis(m,1)).eq.'HOH'.and.resname(hstru(o,l)).eq.'HOH
              ') &
                  hbondi(ncvlu,6)=hbondi(ncvlu,6)+1
          if (resname(hblis(m,1)).eq.'C6H'.and.resname(hstru(o,l)).eq.'HOH'
              ) hbondi(ncvlu,5)&
                  =hbondi(ncvlu,5)+1
    do n=1,indez(1)
       if (resseq(clusts(n)).eq.resseq(hblis(m,1))) then
          nam(molecule)=nam(molecule)+1
          hstru(molecule,nam(molecule))=clusts(n)
       endif
    end do
  endif
 end do
 end do
228 continue
end do
!
!


if (hbondi(ncvlu,2).eq.0.and.hbondi(ncvlu,3).eq.0.and.&
    hbondi(ncvlu,4).eq.0.and.hbondi(ncvlu,5).eq.0.and.&
    hbondi(ncvlu,6).eq.0) then
!   strange structure
          do m=2,6
            hbondi(ncvlu,m)=0
          end do
          hbondi(ncvlu,9)=1
```

```
elseif (hbondi(ncvlu,2).eq.2.and.hbondi(ncvlu,3).eq.0.and.&
        hbondi(ncvlu,4).eq.0.and.hbondi(ncvlu,5).eq.0.and.&
        hbondi(ncvlu,6).eq.0) then
        hbondi(ncvlu,29)=1
        ! bridge doppio
elseif (hbondi(ncvlu,2).eq.2.and.hbondi(ncvlu,3).eq.0.and.&
        hbondi(ncvlu,4).eq.0.and.hbondi(ncvlu,5).eq.0.and.&
        hbondi(ncvlu,6).eq.1) then
        hbondi(ncvlu,34)=1
        ! bridge doppio con acqua
elseif (hbondi(ncvlu,2).eq.2.and.hbondi(ncvlu,3).eq.0.and.&
        hbondi(ncvlu,4).eq.1.and.hbondi(ncvlu,5).eq.0.and.&
        hbondi(ncvlu,6).eq.0) then
hbondi(ncvlu,30)=1
elseif (hbondi(ncvlu,2).eq.2.and.hbondi(ncvlu,3).eq.0.and.&
        hbondi(ncvlu,4).eq.1.and.hbondi(ncvlu,5).eq.0.and.&
        hbondi(ncvlu,6).eq.1) then
hbondi(ncvlu,31)=1
elseif (hbondi(ncvlu,2).eq.2.and.hbondi(ncvlu,3).eq.0.and.&
        hbondi(ncvlu,4).eq.1.and.hbondi(ncvlu,5).eq.1.and.&
        hbondi(ncvlu,6).eq.0) then
hbondi(ncvlu,32)=1
elseif (hbondi(ncvlu,2).eq.2.and.hbondi(ncvlu,3).eq.0.and.&
        hbondi(ncvlu,4).eq.1.and.hbondi(ncvlu,5).eq.1.and.&
        hbondi(ncvlu,6).eq.1) then
hbondi(ncvlu,33)=1

elseif (hbondi(ncvlu,2).eq.1.and.hbondi(ncvlu,3).eq.0.and.&
        hbondi(ncvlu,4).eq.0) then
!   bridge
          do m=2,6
            hbondi(ncvlu,m)=0
          end do
          hbondi(ncvlu,10)=1

elseif (hbondi(ncvlu,2).eq.1.and.hbondi(ncvlu,3).eq.0.and.&
        hbondi(ncvlu,4).eq.1.and.hbondi(ncvlu,5).eq.0.and.&
        hbondi(ncvlu,6).eq.0) then
        hbondi(ncvlu,11)=1
!   strange bridge−water
elseif (hbondi(ncvlu,2).eq.1.and.hbondi(ncvlu,3).eq.0.and.&
        hbondi(ncvlu,4).eq.1.and.hbondi(ncvlu,5).eq.0.and.&
        hbondi(ncvlu,6).eq.1) then
hbondi(ncvlu,12)=1
elseif (hbondi(ncvlu,2).eq.1.and.hbondi(ncvlu,3).eq.0.and.&
        hbondi(ncvlu,4).eq.1.and.hbondi(ncvlu,5).eq.1.and.&
        hbondi(ncvlu,6).eq.0) then
hbondi(ncvlu,13)=1
elseif (hbondi(ncvlu,2).eq.1.and.hbondi(ncvlu,3).eq.0.and.&
```

```
          hbondi(ncvlu,4).eq.1.and.hbondi(ncvlu,5).eq.1.and.&
          hbondi(ncvlu,6).eq.1) then
hbondi(ncvlu,14)=1
!           do m=2,6
!             hbondi(ncvlu,m)=0
!           end do

elseif  (hbondi(ncvlu,2).eq.1.and.hbondi(ncvlu,3).eq.1.and.&
          hbondi(ncvlu,4).eq.0.and.hbondi(ncvlu,5).eq.0.and.&
          hbondi(ncvlu,6).eq.0) then
!    non chemical bridge-water
            hbondi(ncvlu,15)=1
elseif  (hbondi(ncvlu,2).eq.1.and.hbondi(ncvlu,3).eq.1.and.&
          hbondi(ncvlu,4).eq.0.and.hbondi(ncvlu,5).eq.0.and.&
          hbondi(ncvlu,6).eq.1) then
          hbondi(ncvlu,34)=1
elseif  (hbondi(ncvlu,2).eq.1.and.hbondi(ncvlu,3).eq.1.and.&
          hbondi(ncvlu,4).eq.0.and.hbondi(ncvlu,5).eq.1.and.&
          hbondi(ncvlu,6).eq.0) then
          hbondi(ncvlu,35)=1
elseif  (hbondi(ncvlu,2).eq.1.and.hbondi(ncvlu,3).eq.1.and.&
          hbondi(ncvlu,4).eq.0.and.hbondi(ncvlu,5).eq.1.and.&
          hbondi(ncvlu,6).eq.1) then
          hbondi(ncvlu,36)=1

elseif  (hbondi(ncvlu,2).eq.1.and.hbondi(ncvlu,3).eq.1.and.&
          hbondi(ncvlu,4).eq.1) then
!    non chemical bridge-water
            hbondi(ncvlu,16)=1
          do m=2,6
            hbondi(ncvlu,m)=0
          end do

elseif  (hbondi(ncvlu,2).eq.0.and.hbondi(ncvlu,3).eq.1.and.hbondi(ncvlu,4).
     eq.0.and.&
          hbondi(ncvlu,5).eq.0.and.hbondi(ncvlu,6).eq.0) then
hbondi(ncvlu,17)=1
!    water-water III
elseif  (hbondi(ncvlu,2).eq.0.and.hbondi(ncvlu,3).eq.1.and.hbondi(ncvlu,4).
     eq.0.and.&
          hbondi(ncvlu,5).eq.0.and.hbondi(ncvlu,6).eq.1) then
hbondi(ncvlu,18)=1
elseif  (hbondi(ncvlu,2).eq.0.and.hbondi(ncvlu,3).eq.1.and.hbondi(ncvlu,4).
     eq.0.and.&
          hbondi(ncvlu,5).eq.1.and.hbondi(ncvlu,6).eq.0) then
hbondi(ncvlu,19)=1
elseif  (hbondi(ncvlu,2).eq.0.and.hbondi(ncvlu,3).eq.1.and.hbondi(ncvlu,4).
     eq.0.and.&
          hbondi(ncvlu,5).eq.1.and.hbondi(ncvlu,6).eq.1) then
hbondi(ncvlu,20)=1
```

```
elseif (hbondi(ncvlu,2).eq.0.and.hbondi(ncvlu,3).eq.1.and.hbondi(ncvlu,4).
     eq.1.and.&
         hbondi(ncvlu,5).eq.0.and.hbondi(ncvlu,6).eq.0) then
hbondi(ncvlu,21)=1
!   water−water III−IV
elseif (hbondi(ncvlu,2).eq.0.and.hbondi(ncvlu,3).eq.1.and.hbondi(ncvlu,4).
     eq.1.and.&
         hbondi(ncvlu,5).eq.0.and.hbondi(ncvlu,6).eq.1) then
hbondi(ncvlu,22)=1
elseif (hbondi(ncvlu,2).eq.0.and.hbondi(ncvlu,3).eq.1.and.hbondi(ncvlu,4).
     eq.1.and.&
         hbondi(ncvlu,5).eq.1.and.hbondi(ncvlu,6).eq.0) then
hbondi(ncvlu,23)=1
elseif (hbondi(ncvlu,2).eq.0.and.hbondi(ncvlu,3).eq.1.and.hbondi(ncvlu,4).
     eq.1.and.&
         hbondi(ncvlu,5).eq.1.and.hbondi(ncvlu,6).eq.1) then
hbondi(ncvlu,24)=1

elseif (hbondi(ncvlu,2).eq.0.and.hbondi(ncvlu,3).eq.0.and.hbondi(ncvlu,4).
     eq.1.and.&
         hbondi(ncvlu,5).eq.0.and.hbondi(ncvlu,6).eq.0) then
hbondi(ncvlu,25)=1
!   water−water IV
elseif (hbondi(ncvlu,2).eq.0.and.hbondi(ncvlu,3).eq.0.and.hbondi(ncvlu,4).
     eq.1.and.&
         hbondi(ncvlu,5).eq.0.and.hbondi(ncvlu,6).eq.1) then
hbondi(ncvlu,26)=1
elseif (hbondi(ncvlu,2).eq.0.and.hbondi(ncvlu,3).eq.0.and.hbondi(ncvlu,4).
     eq.1.and.&
         hbondi(ncvlu,5).eq.1.and.hbondi(ncvlu,6).eq.0) then
hbondi(ncvlu,27)=1
elseif (hbondi(ncvlu,2).eq.0.and.hbondi(ncvlu,3).eq.0.and.hbondi(ncvlu,4).
     eq.1.and.&
         hbondi(ncvlu,5).eq.1.and.hbondi(ncvlu,6).eq.1) then
hbondi(ncvlu,28)=1
endif

goto 232
230 continue

 if (hbondi(ncvlu,37).eq.1) then

do k=1,2
do l=1,nam(k)
  do m=1,hbo
  if (hblis(m,1).eq.hstru(k,l)) then
          do o=1,molecule
           do p=1,nam(o)
            if (resseq(hblis(m,2)).eq.resseq(hstru(o,p))) goto 231
```

```
          end do
        end do
  molecule=molecule+1
    if (resname(hblis(m,2)).eq.'HOH'.and.k.eq.1) then
      if (atname(hblis(m,2)).eq.'␣O␣␣') hbondi(ncvlu,38)=hbondi(ncvlu
        ,38)+1
      if (atname(hblis(m,1)).eq.'␣O␣␣') hbondi(ncvlu,39)=hbondi(ncvlu
        ,39)+1
    elseif (resname(hblis(m,2)).eq.'HOH'.and.k.eq.2) then
        if (atname(hblis(m,2)).eq.'␣O␣␣') hbondi(ncvlu,40)=hbondi(ncvlu
          ,40)+1
        if (atname(hblis(m,1)).eq.'␣O␣␣') hbondi(ncvlu,41)=hbondi(ncvlu
          ,41)+1
    elseif (resname(hblis(m,2)).eq.'C6H'.and.k.eq.1) then
          hbondi(ncvlu,39)=hbondi(ncvlu,42)+1
    elseif (resname(hblis(m,2)).eq.'C6H'.and.k.eq.1) then
          hbondi(ncvlu,39)=hbondi(ncvlu,43)+1
    endif
   do n=1,indez(1)
      if (resseq(clusts(n)).eq.resseq(hblis(m,2))) then
        nam(molecule)=nam(molecule)+1
        hstru(molecule,nam(molecule))=clusts(n)
      endif
   end do
elseif (hblis(m,2).eq.hstru(k,1)) then
        do o=1,molecule
         do p=1,nam(o)
          if (resseq(hblis(m,1)).eq.resseq(hstru(o,p))) goto 231
         end do
        end do
  molecule=molecule+1
    if (resname(hblis(m,1)).eq.'HOH'.and.k.eq.1) then
      if (atname(hblis(m,1)).eq.'␣O␣␣') hbondi(ncvlu,44)=hbondi(ncvlu
        ,44)+1
      if (atname(hblis(m,2)).eq.'␣O␣␣') hbondi(ncvlu,45)=hbondi(ncvlu
        ,45)+1
    elseif (resname(hblis(m,1)).eq.'HOH'.and.k.eq.2) then
        if (atname(hblis(m,1)).eq.'␣O␣␣') hbondi(ncvlu,46)=hbondi(ncvlu
          ,46)+1
        if (atname(hblis(m,2)).eq.'␣O␣␣') hbondi(ncvlu,47)=hbondi(ncvlu
          ,47)+1
    elseif (resname(hblis(m,1)).eq.'C6H'.and.k.eq.1) then
          hbondi(ncvlu,39)=hbondi(ncvlu,48)+1
    elseif (resname(hblis(m,1)).eq.'C6H'.and.k.eq.1) then
          hbondi(ncvlu,39)=hbondi(ncvlu,49)+1
    endif
  do n=1,indez(1)
      if (resseq(clusts(n)).eq.resseq(hblis(m,1))) then
        nam(molecule)=nam(molecule)+1
        hstru(molecule,nam(molecule))=clusts(n)
```

```
        endif
      end do
    endif
231 continue
 end do
end do
end do




endif

232 continue

!write(6,*) hbondi(ncvlu,:),molecule
write(11,*) molecule,hbondi(ncvlu,:)
!do l=1,molecule
!do m=1,nam(l)
!write(6,*)   molecule,hstru(l,m)
!end do
!end do

! End Of Writing the cluster coordinates
      deallocate(clustn,clust, irstru )
      deallocate(clusts,hblis )
      deallocate(dlist, alist )

          end if

   end do
      deallocate(rij)
      deallocate(px)
      deallocate(fx)
end do

do i=1,49
 do j=1,ncvlu
  repro(i,1)=repro(i,1)+hbondi(j,i)
 end do
end do

repro(1,2)=(repro(1,1))

do i=2,49
repro(i,2)=(repro(i,1)/repro(1,1))*100
end do
```

```
do j=1,49
write(11,*) 'STRUCTURE', j, repro(j,2)
end do


219 write(6,*) 'JOB COMPLETED'

deallocate(hbondi,hbond)
deallocate(serial,atname,altloc,resname,chainid,resseq,icode,occ,tempf,
     element,charge)
deallocate(hlist,hdist)

close(1)
close(9)
close(2)
close(3)
close(4)
close(8)
close(11)

stop
end

!       SUBROUTINE SUBRAY(p,RAY)
!       INTEGER NMAX,l, o,logi,coun
!       PARAMETER (NMAX=3000)
!       CHARACTER*4 p, ATMSYM(NMAX)
!       REAL RAY, RAYC(NMAX)
!112   format(a4,1x,f4.2)
!113   format(a4,1x,a4,1x,f4.2,1x,f4.2)
!114   format(a4,1x,f4.2)
!       OPEN(10, FILE='RAYCOV', STATUS='OLD')
!       coun=0
!!       write(6,114) p,ray
!       DO 201 l=1,NMAX
!       READ(10,112,END=202) ATMSYM(l), RAYC(l)
!       coun=coun+1
!201   CONTINUE
!202   CONTINUE
!       CLOSE(10)
!       logi=0
!       DO 200 o=1,coun
!         IF (p==ATMSYM(o)) THEN
!           RAY = RAYC(o)
!           logi = 1
!           goto 203
!        ENDIF
!
!200   CONTINUE
```

```
!       if (logi.eq.0) write(6,*) p,ATMSYM(1),RAYC(l),RAY
!203    continue
!       RETURN
!       END

     105,1          Fon
```

Bibliography

[1] C. Adamo and V. Barone, 1997.

[2] G. Scherillo at al. Thermodynamics of water sorption in poly(ε-caprolactone): A comparative analysis of lattice fluid models including hydrogen bond contributions, 2012.

[3] G. B. Bachelet, D. R. Hamann, and M. Schluter, 1982.

[4] A. D. Becke, 1988.

[5] A. D. Becke, 1993.

[6] H. BITTIGER, R. H. MARCHESSAULT, and W. O. NIEGISCH. Crystal structure of poly-$\varepsilon-$caprolactone, 1969.

[7] F. Bloch. Über die quantenmechanik der elektronen in kristallgittern, 1928.

[8] S.F. Boys, 1950.

[9] C. G. Broyden. The convergence of a class of double-rank minimization algorithms 1. general considerations., 1970.

[10] C. G. Broyden. The convergence of a class of double-rank minimization algorithms 1. the new algorithm., 1970.

[11] I.G. Economou C. Panayiotou, I. Tsivintzelis, 2007.

[12] I.C. Sanchez C. Panayiotout. Hydrogen bonding in fluids:an equation-of-state approach, 1991.

[13] Alder Ceperly, 1980.

[14] G. O. Arbman D. D. Koelling, 1975.

[15] E. de Paz, A. Martin, S. Rodriguez-Rojo, J. Herreras, and M. J. Cocero, 2010.

[16] D.A. Kleier et al., 1974.

[17] R. Fletcher, 1970.

[18] P. J. Flory, 1942.

[19] P. J. Flory. Principles of polymer chemistry, 1942.

[20] M. Galizia, P. La Manna, G. Mensitieri, M. Panico, and P. Musto. Diffusion in polymers as investigated by two-dimensional correlation spectroscopy: The h_2o/pcl system, 2014.

[21] D. Goldfarb, 1970.

[22] G. Gorrasi, M. Tortora, V. Vittoria, E. Pollet, B. Lepoittevin, and A. P. Dubois, 2003.

[23] E. A. Guggenheim. Mixtures, 1952.

[24] D. R. Hamann, M. Schluter, and C. Chiang, 1979.

[25] M. L. Huggins. Theory of solutions of high polymers, 1942.

[26] M. L. Huggins. Thermodumanic properties of solutions of long-chain compounds, 1942.

[27] C. Panayiotou I. C. Sanchez. Equations of state thermodynamics of polymer and related solutions., 1994.

[28] R. H. Lacombe I. C. Sanchez. An elementary molecular theory of classical fluids., 1976.

[29] J. m. Bofilll J. M. Anglada, 1998.

[30] M. Ernzerhof J. P. Perdew, K. Burke, 1996.

[31] G. P. Kerker, 1980.

[32] Jeffery B. Klauda, Richard M. Venable, J. Alfredo Freites, Joseph W. O'Connor, Douglas J. Tobias, Carlos Mondragon-Ramirez, Igor Vorobyov, Jr. Alexander D. MacKerell, and Richard W. Pastor. Update of the charmm all-atom additive force field for lipids: Validation on six lipid types, 2010.

[33] J. Korringa, 1947.

[34] Parr Lee, Yang, 1988.

[35] Levy, 1982.

[36] G. E. Scuseria M. Ernzerhof, 1999.

[37] B. H. Park M. S. Yeom, K. Yoo, 1999.

[38] W. Kohn P. Hohenberg, 1964.

[39] R. A. Orwoll P. J. Flory and A. Vrij, 1964.

[40] J. P. Perdew, J. A. Chervary, S. H. Vosko, K. A. Jackson, M. R. Pederson, D. J. Singh, and C. Fiolhais, 1992.

[41] G. S. Rushbrooke R. H. Fowler. Non ideality of regular mixtures, 1937.

[42] M. Schlenkrich, J. Brickmann, A.D. MacKerell, Jr., and M. Karplus. Empirical potential energy function for phospholipids: Criteria for parameter optimization and applications, in "biological membranes: A molecular perspective from computation and experiment, 1996.

[43] D. F. Shanno, 1970.

[44] J. C. Slater, 1952.

[45] A. J. Staverman. The entropy of hight polymer solutions. generalization of formulae, 1950.

[46] M. Tortora, V. Vittoria, G. Galli, S. Ritrovati, and E. Chiellini, 2002.

[47] N. Troullier and J. L. Martins, 1990.

[48] F. B. van Duijneveldt, J. G. C. M. van Duijneveldt-van de Rijdt, and J. H. van Lenthe, 1994.

[49] D. Vanderbilt, 1985.

[50] M. Vert, J. Feijen, A. C. Albertsson, G. Scott, and E. Chiellini, 1992.

[51] B. A. Veytsman, 1990.

[52] web. Nist webbook of chemistry, 2016.

[53] H.W. Siesler Y. Peng, P. Wu, 2003.

[54] C. W. YONG. Udff file for dlfield version 3.0 onwards, 2013.

[55] A. Zunger and M. L. Cohen, 1978.